

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 27, 2003, 20:11:16 ; Search time 5026 Seconds

(without alignments)
10752.411 Million cell updates/sec

Title: us-09-934-249-1

Perfect score: 1321

Sequence: 1 cgaaccgcgcgtctcgagcga.....ctgcgtagtgtaaaagcag 1321

Scoring table: OLIGO_NUC

Gapop 60.0, Gapext 60.0

Searched: 2888711 seqs, 20454813386 residues

Database size: 8

Total number of hits satisfying chosen parameters: 4535150

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl.*

1: gb_da.*

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3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

15: em_da.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vl.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rnd.*

36: em_htg_mam.*

37: em_htg_vtl.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1321	100.0	1321	6	AX392417 Sequence
2	1229	93.0	4839	6	AF305616 Homo sapi
3	861	65.2	861	6	AX392419 Sequence
4	838	63.4	1061	9	BC015918 Homo sapi
5	800	60.6	1141	9	AF224278 Homo sapi
6	800	60.6	1818	9	AV128643 Homo sapi
7	593	44.9	61505	9	AF305426 Homo sapi
8	593	44.9	130435	9	HS171817 Homo sapi
9	560	42.4	1583	6	AX593655 Human DNA
10	521	39.4	150224	9	HS0105917 Human DNA
11	401	30.4	408	6	AX071267 Sequence
12	302	22.9	693	6	AX392430 Sequence
13	271	20.5	812	6	AX011709 Sequence
14	51	3.9	51	6	AX199565 Sequence
15	44	3.3	651	10	AF220208 Mus muscu
16	44	3.3	878	6	AX392428 Sequence
17	44	3.3	1379	10	BC036995 Mus muscu
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19	44	3.3	175754	2	AC110189 Mus muscu
20	44	3.3	176458	2	AC134911 Mus muscu
21	44	3.3	176821	2	AL837520 Mus muscu
22	42	3.2	673	6	AX525744 Sequence
23	42	3.2	249554	2	AC139417 Rattus no
24	42	3.2	258632	2	AC111878 Rattus no
25	41	3.1	475	6	AX392431 Sequence
26	41	3.1	175754	2	AC110189 Mus muscu
27	37	2.8	175363	2	AC116815 Mus muscu
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35	34	2.6	198689	2	AC126463 Rattus no
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37	34	2.6	221100	2	AC112841 Rattus no
38	34	2.6	233939	2	AC105853 Rattus no
39	34	2.6	237026	2	AC103439 Rattus no
40	34	2.6	237151	2	AC137424 Rattus no
41	34	2.6	242493	2	AC137322 Rattus no
42	34	2.6	247356	2	AC111257 Rattus no
43	34	2.6	266344	9	AC005158 Homo sapi
44	34	2.6	275229	2	AC098198 Rattus no
45	34	2.6	305075	2	AC106355 Rattus no

ALIGNMENTS

RESULT 1

AX392417 LOCUS

DEFINITION

AX392417 Sequence 1 from Patent WO0216416.

ACCESSION

AX392417

VERSION

AX392417.1 GI:19700732

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

1 Lee, R.T., Landschulz, K.T., Kennedy, S.P., Thompson, J.F. and Turi, T.G.

Diagnosis and treatment of cardiovascular conditions

Pred. No. is the number of results predicted by chance to have a

JOURNAL Patent: WO 0216416-A.1 28-FEB-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; PFIZER INC. (US)

FEATURES Location/Qualifiers
source 1.1321

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/note="unnamed protein product"
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/db_xref="gi:1970073"

BASE COUNT 223 a 493 c 440 g 165 t

Very Match 100.0%; Score 1321; DB 6; Length 1321;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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961 GCG 1020
961 GCG 1020
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1201 CAC 1260
1201 CAC 1260
1261 AGGACACCGCTCTGAGGCTCCCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1320
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1321 G 1321
1321 G 1321

RESULT 2

AF305616 4839 bp mRNA linear PRI 21-OCT-2001

LOCUS Homo sapiens STAG1/PMEPA1 mRNA, complete cds.
DEFINITION AF305616
VERSION AF305616.1 GI:16303741
KEYWORDS

SOURCE ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 4839)
Rae,F.K., Hooper,J.D., Nicol,D.L. and Clements,J.A.

Characterization of a novel gene, STAG1/PMEPA1, upregulated in renal cell carcinoma and other solid tumors
Mol. Cell. Oncol. 32 (1), 44-53 (2001)

JOURNAL MEDLINE 21453682
PUBMED 11568975

REFERENCE 2 (bases 1 to 4839)
Rae,F.K., Hooper,J.D., Nicol,D.L. and Clements,J.A.

Direct Submission
Submitted (14-SEP-2000) Centre for Molecular Biotechnology,
Queensland University of Technology, 2 George St, Brisbane, QLD
4001, Australia

FEATURES Location/Qualifiers
source 1..4839
/organism="Homo sapiens"
/mol_type="mRNA"

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Db	700	GCCACTACCCGGGGTCTCTCTTCCAGCACACAGACAGATGGGGCGCCCTCTCTTGGCTGG	759
Qy	1182	AGGGACCCGGCTCCACCACACACATCGGCCCTTAGAGAGGCGCATTCTGGAGCA	1241
Db	760	AGGGGACCCGGCTCCACCACACACATCGGGCCCTTAGAGAGGCGCATTCTGGAGCA	819
Qy	1242	AAGAGAAAGATTAACAGAAAGAACCTCTCTTAGGTGCCCCAGGGGGCGGGGCTGGGG	1301
Db	820	AAGAGAAAGATTAACAGAAAGAACCTCTCTTAGGTGCCCCAGGGGGCGGGGCTGGGG	879
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Db	880	CTGCCTAGGTGAAAAAGCAGC	899

RESULTS	1818 bp	mRNA	linear	PRI 10-APR-2003
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DEFINITION	AY128643.1	GI:22121998		
ACCESSION				
VERSION				
KEYWORDS				
SOURCE	Hom sapiens (human)			

ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE AUTHORS	1 (bases 1 to 1818) Brunschwig, E.B., Wilson, K., Mack, D., Dawson, D., Lawrence, E., S. Morrell, A., Davis, P.M., Schiller, S., Beard, L.,

TITLE
terminal colonocyte differentiation whose expression is maintained
in primary and metastatic colon cancer
Cancer Res. 63 (7), 1566-1575 (2003)

MEDLINE	22557253
PubMed	12670906
REFERENCE	
AUTHORS	2 (bases 1 to 1818) Brunschwig, E.B., Wilson, K., Mack, D., Dawson, D., Lawrence, E., Wilson, J.K.V., Lu, S., Nostri, A., Swiner, S., Beard, L., Luttrebaugh, J.D., Willis, J., Platzer, P. and Markowitz, S.
TITLE	Direct Submersion
JOURNAL	Submitted (03-JUL-2002) Department of Medicine, Case Western Reserve University/Howard Hughes Medical Institute, 11001 Cedar Ave., Cleveland, OH 44106, USA

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[illegible]

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QY	882	ATCCGCCACACCTTACACAGGGGCCCTTGCACCCCTTCACGCTTTCGGGACCCCGAGCAGCAGCTGG	941
Db	464	ATCCGCCACACCTTACACAGGGGCCCTTGCACCCCTTCACGCTTTCGGGACCCCGAGCAGCAGCTGG	523
QY	942	AACTGTAACCGGAGTTCGTGGCGCGCACCCCAACAGAACCATCTTGCACAGTGAAGCTGA	1001

Db	524	AACTGAAACCGGAGTGCCTGCGCCACCCCAACAGACGACCATCTTGACAGTCACTCGA	583
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Qy	1062	CGTGTACTACGGCAGCGCGGCGGCATGAGAGGGCGCGCCCACTTACAGCGAGGTCAATCG	1121
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AF305426	61505 bp	DNA	linear	PRI 12-OCT-2001
LOCUS	AF305426	61505	bp	
DEFINITION	Homo sapiens solid tumor-associated 1 protein (STAG1/PMEPA1) gene, complete cds.			
ACCESSION	AF305426			
VERSION	AF305426.1	GI:15824468		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			

REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
1	(bases 1 to 61505)
Rae, F. K., Hooper, J. D., Nicol, D. L. and Clements, J. A.	
Identification and characterization of a novel gene, SMAG1,	
up-regulated in renal cell carcinoma and other solid tumours	
Unpublished	

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repeat_region	2028. .2632	/note="11 copies 55 mer 60% conserved"
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repeat_region	5797. .5988	/note="6 copies 32 mer 86% conserved"
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repeat_region	6592. .6723	/note="FLAM_C repeat: matches 1. .132 of consensus"
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15021..15110
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15026..15109
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15420..15721
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18049..18169
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/note="16 copies 2 mer tc 87% conserved"
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27603..27684
/note="12 repeat: matches 2661..2739 of consensus"
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/note="MIR repeat: matches 38..242 of consensus"
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128443 AGCGCAGGTCTACGCCCGCTGCGCCACGACGCGCTGGCGCGTGGCCCTTGCC 128384
|||||
789 AGCGGAGGCGCTTCCACGCGCTTCCAGCCACGACCTATCCGTACTCGACGACAGAGATGACC 848
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128383 AGCGGAGGCGCTTCCACGCGCTTCCAGCCACGACCTATCCGTACTCGACGACAGAGATGACC 128324
|||||

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as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP5-1059L7 is from the library RPc1-5 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>
VECTOR: pCYPAC2.

FEATURES
Location/Qualifiers

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1509..1628
repeat_region
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2076..2155
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/db_xref="GI:13160408"
/translation="MALEFVQIIIVVMVWVITCLSHYKLSARSFISRHSGRRREDALSS"
complement(join(<2445..2599,52376..52477))
/feature="TMEPAI"
/product="dJ1059L7.1.1 (androgen induced type 1b transmembrane protein (PMEPAI), isoform 1)"
/feature="match: CDNAS: Em:AF009426 Em:AF009427 Em:AF009425 Em:AF009424"
match: ESTs: Em:AA249792 Em:AI594390 Em:AA128075 Em:AA088767
evidence=not_experimental
complement(join(<2445..2599,52376..52472))
/feature="TMEPAI"
/feature="continues in dJ718J7 (AL035541)"
match: proteins: Tr:O15166 Tr:O15168"
/codon_start=1
evidence=not_experimental
/product="dJ1059L7.1.1 (androgen induced type 1b transmembrane protein (PMEPAI), isoform 1)"
/protein_id="CAB88144.1"
/db_xref="GI:7619746"
/db_xref="SPTREMBL:Q9NTR9"
/translation="MGVNSTAAAGAPVNSCTCNCKRSLFQSMETLEFVQIIIVVMVWVITCLSHYKLSARSFISRHSGRRREDALSS"
2538..2567
repeat_region
/feature="L2 repeat: matches 3 mer cac 90% conserved"
3128..3606
misc_feature
/feature="match: GSS: Em:AQ059507"
3214..3324
repeat_region
/feature="L2 repeat: matches 37 mer 83% conserved"
3339..3413
repeat_region
/feature="L2 repeat: matches 25 mer 92% conserved"
3390..3921
repeat_region
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/note="19 copies 28 mer 61% conserved"
3394..3893
repeat_region
/feature="L2 repeat: matches 25 copies 20 mer 59% conserved"
3407..3892
repeat_region
/feature="L2 repeat: matches 27 copies 18 mer 58% conserved"
3421..3910
repeat_region
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3473..3904
repeat_region
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3553..3932
repeat_region
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3573..3697
repeat_region
/feature="L2 repeat: matches 25 mer 76% conserved"
3746..3921
repeat_region
/feature="L2 repeat: matches 22 mer 64% conserved"
4032..4069
repeat_region
/feature="L2 repeat: matches 2 mer 81% conserved"
4792..5001
repeat_region
/feature="L2 repeat: matches 3 copies 70 mer 82% conserved"
5002..5190
repeat_region
/feature="L2 repeat: matches 1..200 of consensus"
5224..5282
repeat_region
/feature="L2 repeat: matches 94..154 of consensus"
8103..8205
repeat_region
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complement(858..9277)
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/feature="match: GSS: Em:AQ881699"
9224..9382
repeat_region
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9286..9706
misc_feature
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9295..9861
misc_feature
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10035..10140
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11175..11343
repeat_region
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11630..12037
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12054..12362
repeat_region
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14448..14493
repeat_region
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14634..14813
repeat_region
/feature="L2 repeat: matches 1..187 of consensus"
15096..15497
misc_feature
/feature="CPG island"
evidence=not_experimental
15690..15935
repeat_region
/feature="L2 repeat: matches 7..254 of consensus"
15989..17387
repeat_region
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17647..17703
repeat_region
/feature="L2 repeat: matches 2679..2736 of consensus"
17699..18179
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17902..18039
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repeat_region
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19954..20005
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20264..20432
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/feature="L2 repeat: matches 2581..2750 of consensus"
20530..21282
repeat_region
/feature="L2 repeat: matches 5595..6341 of consensus"
21980..22192
repeat_region
/feature="L2 repeat: matches 2332..2562 of consensus"
23102..23203
repeat_region
/feature="L2 repeat: matches 117..218 of consensus"
23231..23438
repeat_region
/feature="L2 repeat: matches 3..218 of consensus"
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repeat_region 23439..23512
/note="MIR repeat: matches 182..257 of consensus"
repeat_region 24460..24580
/note="L1MD1 repeat: matches 6102..6221 of consensus"
repeat_region 24752..25042
/note="L2 repeat: matches 2386..2709 of consensus"
repeat_region 25208..25295
/note="MIR repeat: matches 61..155 of consensus"
repeat_region 26450..26485
/note="18 copies 2 mer tg 97% conserved"
repeat_region 29374..29501
/note="MIR repeat: matches 55..190 of consensus"
repeat_region 29550..29728
/note="MIR repeat: matches 69..248 of consensus"

Query Match 39.4%; Score 521; DB 9; Length 15024;
Best Local Similarity 100.0%; Pred. No. 1.7e-257; Mismatches 0; Indels 0; Gaps 0;
Matches 521; Conservative 0;

1 CGACCGCGGTCTCGAGCGAAACCGATCTCTTGTTCAGATGAGAGAGAGAGCGG 60
CGACCGCGGTCTCGAGCGAAACCGATCTCTTGTTCAGATGAGAGAGAGAGCGG 52837

61 CG 120
CG 52777

121 GCGCGCAGCG 180
GCGCGCAGCG 52717

52716 GCGCGCAGCG 52717

181 AGCG 240
AGCG 52657

52716 AGCG 52657

241 TGAGCG 300
TGAGCG 52597

52596 TGAGCG 52597

301 CTCGCCCG 360
CTCGGCCG 52537

52536 CTCGCCCG 52537

361 CCG 420
CCG 52477

52536 CCG 52477

421 CTGATGGGGGTCAACAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
CTGATGGGGGTCAACAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 52417

52476 CTGATGGGGGTCAACAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 52417

481 GTGCAACTGCAAAACGCTCTTGTTCAGAGCATGAGATCA 521
GTGCAACTGCAAAACGCTCTTGTTCAGAGCATGAGATCA 52376

52416 GTGCAACTGCAAAACGCTCTTGTTCAGAGCATGAGATCA 52376

RESULT 11
AX071267 408 bp DNA linear PAR 25-JAN-2001
LOCUS AX071267
DEFINITION Sequence 1739 from Patent WO0102568.
ACCESSION AX071267
VERSION AX071267.1 GI:12581618
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS 1 Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klingner, J., Kasam, A., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot, D., Lamson, G., Drmanac, R., Crkvenjakov, R., Drmanac, S., Dickson, M., Labat, I., Ieshkowitz, D., Kita, D., Garcia, V. and Strache-Crain, B.
Human genes and gene expression products

TITLE

JOURNAL Patent: WO 0102568-A 1739 11-JAN-2001;
CHIRON CORPORATION (US); HYSEQ, INC. (US)
FEATURES
source 1..408
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 81 a 159 c 115 g 53 t
ORIGIN

Query Match 30.4%; Score 401; DB 6; Length 408;
Best Local Similarity 100.0%; Pred. No. 1.7e-195; Mismatches 0; Indels 0; Gaps 0;
Matches 401; Conservative 0;

583 GATCAGTGCCTGCTGAGCAGCACTACAGCTGTCTGACAGCTTCTCATCAGCGGACAG 642
GATCAGTGCCTGCTGAGCAGCACTACAGCTGTCTGACAGCTTCTCATCAGCGGACAG 67

643 CCAGGGGCGGAGAGAGAGATGCTCTGTCTCAGAGAGATGCTGTGCGCTCGAGAG 702
CCAGGGGCGGAGAGAGAGATGCTCTGTCTCAGAGAGATGCTGTGCGCTCGAGAG 127

68 CCAGGGGCGGAGAGAGAGATGCTCTGTCTCAGAGAGATGCTGTGCGCTCGAGAG 127

703 CACAGTGTACAGCAACGAGATCCAGAGCGCGAGCTTACGCGCCCTCGGCGCACCA 762
CACAGTGTACAGCAACGAGATCCAGAGCGCGAGCTTACGCGCCCTCGGCGCACCA 187

763 CCGCGTGGCG 822
CCGCGTGGCG 247

188 CCGCGTGGCG 247

823 TCGTACCTGACAGCAGAGATGACCTGACCCACCAATCTGCTGTGAGAGGGAGGA 882
TCGTACCTGACAGCAGAGATGACCTGACCCACCAATCTGCTGTGAGAGGGAGGA 307

248 TCGTACCTGACAGCAGAGATGACCTGACCCACCAATCTGCTGTGAGAGGGAGGA 307

883 GCCCGCACCTTACAGAGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 942
GCCCGCACCTTACAGAGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 367

308 GCCCGCACCTTACAGAGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 367

943 ACTGAACCGGAGAGTGTGCGCGCACCCCAACAGAACCA 983
ACTGAACCGGAGAGTGTGCGCGCACCCCAACAGAACCA 408

368 ACTGAACCGGAGAGTGTGCGCGCACCCCAACAGAACCA 408

RESULT 12
AX392430 693 bp DNA linear PAR 23-MAR-2002
LOCUS AX392430
DEFINITION Sequence 14 from Patent WO0216416.
ACCESSION AX392430
VERSION AX392430.1 GI:19700746
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS 1 Lee, R.T., Landschulz, K.T., Kennedy, S.P., Thompson, J.F. and Turi, T.G.
Diagnosis and treatment of cardiovascular conditions
Patent: WO 0216416-A 14 28-FEB-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US); PFIZER INC. (US)

FEATURES
source 1..693
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 101 a 205 c 237 g 149 t 1 others
ORIGIN

Query Match 22.9%; Score 302; DB 6; Length 693;
Best Local Similarity 100.0%; Pred. No. 2.5e-144; Mismatches 0; Indels 0; Gaps 0;
Matches 302; Conservative 0;

885 CCCACACCTTACAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 944


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Db      587  |||||CCCCACCTTACAGAGGCGCCCTCGACACCTTCAGCTTGGGAGCCCGAGCAGACCTGGAAC 528
QY      945  TGAACGGGAGTGTGTCGGCGGACCCCAAGCAACATCTTCGACATGACCTATATG 1004
Db      527  |||||TGAACGGGAGTGTGTCGGCGGACCCCAAGCAACATCTTCGACATGACCTATATG 468
QY      1005 ATAGTCCAGAGGTGGCGGCGCCCTGCGCCCGAGCAGTAACTGGGCATCAGCGCCAGT 1064
Db      467  ATAGTCCAGAGGTGGCGGCGCCCTGCGCCCGAGCAGTAACTGGGCATCAGCGCCAGT 408
QY      1065 GCTACGGCAGCGCGCGCGCGCGATGGAGGGCGCGCCCGCCTTACAGCAGGATCATGGCC 1124
Db      407  GCTACGGCAGCGCGCGCGCGCGATGGAGGGCGCGCCCGCCTTACAGCAGGATCATGGCC 348
QY      1125 ACTACCGGGGTCCTCTTCAGCAGCAGCAGAGAGTGGGGCGCGCTCTCTCTGAGG 1184
Db      347  ACTACCGGGGTCCTCTTCAGCAGCAGCAGAGAGTGGGGCGCGCTCTCTCTGAGG 288

1185 GG 1186
287 GG 286

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RESULT 13
LOCUS   AX011709                      812 bp      DNA      linear      PAT 06-SEP-2000
DEFINITION Sequence 107 from Patent WO9955858.
ACCESSION AX011709
VERSION  AX011709.1 GI:9998233
KEYWORDS
SOURCE  Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
          Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and
          Pliarsky,C.
          Human nucleic acid sequences obtained from pancreas tumor tissue
          Patent: WO 9955858-A 107 04-NOV-1999;
          SCHMITT ARMINT (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
          BERND (DE); ROSENTHAL ANDRE (DE); METZGEN GES FUER GENOMFORSCHUN
          (DE); PLIARSKY CHRISTIAN (DE)
FEATURES
          source             1..812
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                           /mol_type="genomic DNA"
                           /db_xref="taxon:9606"

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COUNT 157 a 272 c 237 g 146 t
Query Match      20.5%; Score 271; DB 6; Length 812;
Best Local Similarity 99.7%; Pred. No. 2.7e-128;
Matches 321; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      585  TCACGTGCGCTGCTGACCACTACAGCTGTCTGACAGGTCCTTCATCAGCCGACACCC 644
Db      426  TCACGTGCGCTGCTGACCACTACAGCTGTCTGACAGGTCCTTCATCAGCCGACACCC 485
QY      645  AGGGGGGAGAGAGAAGATGCGCTGCTCAGAGAGATGCGTGGGCGCTCGAGAGCA 704
Db      486  AGGGGGGAGAGAGAAGATGCGCTGCTCAGAGAGATGCGTGGGCGCTCGAGAGCA 545
QY      705  CAGTGTCAAGCAAGCATCCAGAGCCGAGGCTTACGCGCCGCTCGGCCACAGGACC 764
Db      546  CAGTGTCAAGCAAGCATCCAGAGCCGAGGCTTACGCGCCGCTCGGCCACAGGACC 605
QY      765  GCGTGGCGCGCGCGCGCTTGGCGAGGAGCGCTTCCACCGCTTCCAGCCCACTATC 824
Db      606  GCGTGGCGCGCGCGCGCTTGGCGAGGAGCGCTTCCACCGCTTCCAGCCCACTATC 665
QY      825  CGTACCTGACGACGAGATGACCTGCGACCACTCTGCTGACAGCGGGAGGAGG 884

```

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Db      666  CGTACCTGACGACGAGATGACCTGCGCCCGACCATCTGCTGTCCAGAGGGAGGAGCC 725
QY      885  CCCACACCTTACAGGGGCGCCTG 906
Db      726  CCCACACCTTACAGGGGCGCCTG 747

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RESULT 14
LOCUS   AX199565                      51 bp      DNA      linear      PAT 29-AUG-2001
DEFINITION Sequence 495 from Patent WO0151670.
ACCESSION AX199565
VERSION  AX199565.1 GI:15389996
KEYWORDS
SOURCE  Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
          Shinkets,R.A. and Leach,M.D.
          Nucleic acids containing single nucleotide polymorphisms and
          methods of use thereof
          Patent: WO 0151670-A 495 19-JUL-2001;
          Curagen Corporation (US)
FEATURES
          source             1..51
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                           /mol_type="genomic DNA"
                           /db_xref="taxon:9606"

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              /note="1 of 2 allelic variants (496 is other entry)
              Accession number C942747251"
BASE COUNT  12 a 16 c 18 g 5 t
ORIGIN

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Query Match      3.9%; Score 51; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.4e-14;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      618  CACGGTCTTCATCAGCCGCGACAGCGGCGGAGAGAGAGATGCCCC 668
Db      1    CACGGTCTTCATCAGCCGCGACAGCGGCGGAGAGAGAGATGCCCC 51

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RESULT 15
LOCUS   AF220208                      651 bp      mRNA      linear      ROD 05-MAR-2001
DEFINITION Mus musculus Nedd4 WW domain-binding protein 4 mRNA, partial cds.
ACCESSION  AF220208
VERSION  AF220208.1 GI:12004973
KEYWORDS
SOURCE  Mus musculus (house mouse)
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
          1 (bases 1 to 651)
          Jolliffe,C.N., Harvey,K.F., Haines,B.P., Parasivam,G. and Kumar,S.
          Identification of multiple proteins expressed in murine embryos as
          binding partners for the WW domains of the ubiquitin-protein ligase
          Nedd4
          Blochem. J. 351 Pt 3, 557-565 (2000)
JOURNAL  Biochem. J. 351 Pt 3, 557-565 (2000)
MEDLINE  20498735
PUBMED  11042109
REFERENCE 2 (bases 1 to 651)
          Jolliffe,C.N. and Kumar,S.
          Direct Submission
          Submitted (30-DEC-1999) Division of Haematology, Hanson Centre for
          Cancer Research, IMVS, Frome Rd, Adelaide, SA 5000, Australia
          Location/Qualifiers
              1..651
              /organism="Mus musculus"
              /mol_type="mRNA"
              /db_xref="taxon:10090"

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2003, 20:09:06 ; Search time 416 Seconds

(without alignments)
8572.014 Million cell updates/sec

Title: us-09-934-249-1

Perfect score: 1321

Sequence: 1 cgaccgcgcttcgagcgca.....ctgcgtagtgtaaaagcgag 1321

Scoring table:

OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Database size: 8

Total number of hits satisfying chosen parameters: 2877269

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1321	100.0	1321	24	ABK12137 Human cDNA encodin
2	800	60.6	1140	24	ABK92120 Prostate cancer as
3	788	59.7	1066	22	AA157868 Human polynucleoti
4	749	56.7	969	21	AAA75151 cDNA encoding a hu
5	749	56.7	1061	21	AAA47429 Sequence encoding
6	744	56.3	1334	25	AB236103 Human secretory po
7	744	56.3	969	21	AAA75163 cDNA clone encodin
8	698	52.8	969	21	AAA75164 cDNA clone encodin

9	698	52.8	969	21	AAA75165
10	560	42.4	1583	24	AB561424
11	401	30.4	408	22	AAF65983
12	394	29.8	1069	22	AA159654
13	364	27.6	474	25	AB284732
14	302	22.9	693	24	ABK12143
15	271	20.5	812	20	AA252964
16	229	17.3	254	21	AAA41265
17	106	8.0	1879	23	AA584503
18	63	4.8	426	23	AA584502
19	60	4.5	60	24	ABN40872
20	56	4.2	522	24	ABT10027
21	51	3.9	51	22	AAH89714
22	45	3.4	837	24	ABQ43500
23	45	3.4	837	24	ABQ43501
24	44	3.3	878	24	ABK12142
25	44	3.3	1713	21	AAA75152
26	44	3.3	1713	21	AAA75166
27	44	3.3	1713	21	AAA75167
28	44	3.3	1713	21	AAA75168
29	42	3.2	673	24	ABT09178
30	41	3.1	475	24	ABK12144
31	37	2.8	837	24	ABQ43498
32	37	2.8	837	24	ABQ43499
33	34	2.6	640	21	AA565015
34	32	2.4	577	22	ABA50270
35	32	2.4	577	22	ABA68210
36	32	2.4	577	22	ABA35222
37	32	2.4	577	22	AAK16592
38	32	2.4	577	22	AAK42346
39	32	2.4	577	22	AAI23118
40	32	2.4	577	22	AAI48425
41	32	2.4	577	22	AAI08772
42	32	2.4	577	23	AB541955
43	32	2.4	577	24	AB516402
44	32	2.4	1964	22	ABA45134
45	32	2.4	1964	22	ABA55612

ALIGNMENTS

RESULT 1	ABK12137	standard; cDNA; 1321 BP.
XX	ABK12137;	
XX	05-JUN-2002 (first entry)	
XX	Human cDNA encoding Mechanically Induced Vascular Receptor 1, MIVR-1.	
XX	Human; ss: gene; MIVR-1; Mechanically Induced Vascular Receptor 1;	
XX	cytostatic; cardiant; cerebroprotective; antiarteriosclerotic;	
XX	cardiac cell; anti-apoptotic; vascular endothelial cell;	
XX	cardiac hypertrophy; myocardial infarction; stroke; arteriosclerosis;	
XX	heart failure.	
XX	Homo sapiens.	
XX	key	Location/Qualifiers
XX	CDS	413..1276
XX	FT	/*tag= a
XX	FT	/product= "MIVR-1"
XX	FT	/note= "This region is specifically claimed in claim 3"
XX	WO200216416-A2.	
XX	28-FEB-2002.	
XX	21-AUG-2001; 2001WO-US26089.	
XX	22-AUG-2000; 2000US-227159P.	

cDNA clone encodin
Prostate specific
Novel human polynu
Human polynucleoti
Toxicologically re
Human MIVR-1 homol
Human prostate tum
Human secreted exp
DNA encoding novel
DNA encoding novel
Human spliced tran
Human breast cance
Human coding sequ
Oligonucleotide fo
Oligonucleotide fo
Mouse cDNA encodin
cDNA encoding a mu
cDNA clone encodin
cDNA clone encodin
Phase-1 Rat CT gen
Human MIVR-1 homol
Oligonucleotide fo
Oligonucleotide fo
Eucalyptus grandis
Human breast cell
Human foetal liver
Probe #13688 for g
Human brain expres
Human bone marrow
Probe #13051 for g
Probe #17111 used t
Human liver single
Human genome-deriv
Human breast cell
Human foetal liver

[illegible]

OY		1074	GCGGCGGCGCATGATGGAGGGGGCCGCCCAACTTACAGCGAGTCATGCGCACAACC	CGG	1133					
Dd		665	GCGGCGGCGCATGATGGAGGGGGCCGCCCAACTTACAGCGAGTCATGCGCACAACC	CGG	724					
OY		1134	GGTCTCTCTTCCAGCACACAGCAGAGCAGTGGGGGCCCTCTCTTCTGTGAGGGAGCC	CGC	1193					
Dd		725	GGTCTCTCTTCCAGCACACAGCAGAGCAGTGGGGGCCCTCTCTTCTGTGAGGGAGCC	CGC	784					
OY		1194	TTCACACACACACATGCGCGCCCCCTAGAGACGCGAGCATCTGGAGC	AAAGAGAAGATA	1253					
Dd		785	TTCACACACACACATGCGCGCCCCCTAGAGACGCGAGCATCTGGAGC	AAAGAGAAGATA	844					
OY		1254	AACAGAAAAGAGACACCTCTCTTAGGGGTCCCAGGGGGGGCCGTGGGCTCGTAGGTGA		1313					
Dd		845	AACAGAAAAGAGACACCTCTCTTAGGGGTCCCAGGGGGGGCCGTGGGCTCGTAGGTGA		904					
OY		1314	AAAGGCAG	1321						
Dd		905	AAAGGCAG	912						
<hr/>										
RESULT 4										
XX	ID	AAA75151	standard; cDNA; 969 BP.							
XX	AC	AAA75151;								
XX	DT	15-JAN-2001	(first entry)							
DE	XX	cDNA encoding a human TANGO 261 polypeptide.								
KW	XX	TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267;								
KW	XX	cellular proliferation; cellular differentiation; cellular adhesion;								
KW	XX	von Willebrand factor-associated disorder; cell trafficking; cancer;								
KW	XX	hematopoietic associated disease; atelectasis; pulmonary congestion;								
KW	XX	oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;								
KW	XX	intestinal disorder; spleen associated disease; renal disorder;								
KW	XX	cardiovascular disorder; ischemic heart disease; hydrocephalus;								
KW	XX	brain herniation; iatrogenic disease; inflammation; meningitis;								
KW	XX	Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;								
KX	XX	multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.								
<hr/>										
OS	XX	Homo sapiens.								
FH	key	location/Qualifiers								
FT	CDS	6..764								
FT		/tag= a								
FT		/product= "TANGO 261"								
FT	sig_peptide	6..89								
FT		/tag= b								
FT	mat_peptide	90..764								
FT		/tag= c								
PN	WO200052022-A1.									
XX		08-SEP-2000.								
PD		01-MAR-2000; 2000MO-US05226.								
PF		01-MAR-1999; 99US-0122458.								
PA	(MILL-) MILLENNIUM PHARM INC.									
PI	Barnes TM, Holtzman DA, Sharp JD, Fraser CC;									
PI	WPI; 2000-579269/54.									
PB	P-PDB; AAB18449.									
PT	Novel human and murine secreted proteins designated TANGO 216, 261,									
PT	262, 266 and 267 useful as modulating agents of cellular processes,									
PT	e.g. for treating cancer -									
PS	Claim 2; Fig 5; 175pp; English.									

XX The present sequence encodes a human TANGO 261 polypeptide. The
 CC specification also describes TANGO 266, TANGO 216, TANGO 262, and
 CC TANGO 267. The TANGO polypeptides can be used to modulate cellular
 CC proliferation, modulate cellular differentiation and/or modulate
 CC cellular adhesion. The proteins can be used to treat any von Willebrand
 CC factor-associated disorder, regulate extracellular matrix structuring,
 CC cellular adhesion, and cell trafficking and/or migration, modulate
 CC cellular interactions, modulate cell adhesion in proliferative
 CC disorders, such as cancer, modulate the proliferation, differentiation,
 CC and/or function of cells that appear in the bone marrow, and leukocytes,
 CC treat bone marrow, blood and hematopoietic associated diseases and
 CC disorders, atelectasis, pulmonary congestion or oedema, emphysema,
 CC chronic bronchitis, bronchial asthma and bronchiectasis, intestinal
 CC disorders, spleen associated diseases, modulate renal disorders, treat
 CC cardiovascular disorders such as ischemic heart disease, modulate the
 CC proliferation, differentiation, and/or function of bone and cartilage
 CC cells and to treat bone and/or cartilage associated diseases or
 CC disorder. They may also be used to treat disorders associated with the
 CC ovaries, cerebral oedema, hydrocephalus, brain herniations, iatrogenic
 CC disease, inflammation, bacterial and viral meningitis, Alzheimer's
 CC disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis,
 CC brain cancers, hydrocephalus and encephalitis, and treat hepatic
 CC disorders.

50 Sequence 969 BP; 211 A; 316 C; 294 G; 148 T; 0 other;

Query Match 56.7%; Score 749; DB 21; Length 969;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 799; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

522 CGAGCTGAGATTTGTCATGATCATCATCTGTTGGTGTATGATGTTGGTGG 581
 DB 10 CGGAGCTGAGATTTGTCATGATCATCATCTGTTGGTGTATGATGTTGGTGG 69
 582 TGATCAGTGTGCTCTGAGCCATCAAGATGCTGTGACGGTCTCTTATGACCGGCA 641
 DB 70 TGATCAGTGTGCTCTGAGCCATCAAGATGCTGTGACGGTCTCTTATGACCGGCA 129
 642 GCCAGGGGCGAGAGAGAGATGATGCTGTCTCTGAGAGATGCTGTGACCGGCA 701
 DB 130 GCCAGGGGCGAGAGAGATGATGCTGTCTCTGAGAGATGCTGTGACCGGCA 189
 702 GCACAGTGTGACGAGAGATGATGCTGTCTCTGAGAGATGCTGTGACCGGCA 761
 DB 190 GCACAGTGTGACGAGAGATGATGCTGTCTCTGAGAGATGCTGTGACCGGCA 249
 762 ACCGCTGGGCGGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 821
 DB 250 ACCGCTGGGCGGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 309
 822 ATCCGTAATGCTGACAGAGATGATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 881
 DB 310 ATCCGTAATGCTGACAGAGATGATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 369
 882 AGCCGCCACCTTACAGAGGCGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 941
 DB 370 AGCCGCCACCTTACAGAGGCGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 429
 942 AACGTAACCGGAGAGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 1001
 DB 430 AACGTAACCGGAGAGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 489
 1002 TGGATAGTGTGAGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 1061
 DB 490 TGGATAGTGTGAGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 549
 1062 CGTGTGAGGAGGCGGCGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1121
 DB 550 CGTGTGAGGAGGCGGCGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 609
 1122 GCCACTACCGGCGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 1181

DB 610 GCCACTACCGGCGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 669
 1182 AGGGGACCGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1241
 DB 670 AGGGGACCGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 729
 1242 AAGGAAAGATTAACAGAAAGACACCTCTGTAGGTGCTGTGCTGTGCTGTGCT 1301
 DB 730 AAGGAAAGATTAACAGAAAGACACCTCTGTAGGTGCTGTGCTGTGCTGTGCT 789
 1302 CTGCTAGGTGTAAGAGCAG 1321
 DB 790 CTGCTAGGTGTAAGAGCAG 809

RESULT 5

AAAA7429 standard; DNA; 1061 BP.

AAAA7429;

20-OCT-2000 (first entry)

Sequence encoding human neuron-associated protein.

XX Neuron associated protein; NEUP; neurological disorder; epilepsy;
 KW Ischemic cerebrovascular disease; stroke; cerebral neoplasm;
 KW Alzheimer's disease; Pick's disease; Huntington's disease;
 KW dementia; Parkinson's disease; demyelinating disease; meningitis;
 KW prion disease; Kuru; Creutzfeldt-Jakob disease; neurofibromatosis;
 KW cerebral palsy; muscular dystrophy; central nervous system;
 KW peripheral nervous system; PNS; myopathy; schizophrenia;
 KW acinic keratosis; arteriosclerosis; atherosclerosis; bursitis;
 KW cirrhosis; hepatitis; mixed connective tissue disease; MCTD;
 KW myelofibrosis; paroxysmal nocturnal haemoglobinuria; cancer;
 KW autoimmune disease; inflammation; acquired immunodeficiency syndrome;
 KW AIDS; Addison's disease; adult respiratory distress syndrome;
 KW allergy; ankylosing spondylitis; amyloidosis; anaemia; asthma;
 KW Werner syndrome; trauma; human; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT CDS 101..859
 FT /*tag= a
 FT /product= Neuron associated protein

XX WO200034477-A2.

XX 15-JUN-2000.

XX 10-DEC-1999; 99WO-US30408.

XX 11-DEC-1998; 98US-0210083.

XX 11-DEC-1998; 98US-9123456.

XX 09-FEB-1999; 99US-0119365.

XX 16-MAR-1999; 99US-0124687.

XX (INCYTE) INCYTE PHARM INC.

XX Tang YF, Yue H, Baughn MR, Hillman JL, Lai P, Au-young J, Yang J;

XX Lu DAW, Azimzal Y;

XX WPI; 2000-423423/36.

XX P-PSDB; AAB01388.

XX New human neuron-associated proteins and polynucleotides encoding them,
 XX useful for diagnosis, treatment and prevention of cell proliferative
 XX disorders including cancer, neuronal and neurological disorders
 XX Claim 9; Page 136; 145pp; English.
 XX Human neuron-associated proteins (NEUP) can be used for for

XX The invention relates to a secretory polynucleotide (designated spm)
 CC comprising any of 567 polynucleotide sequences (AB235837-AB236403), a
 CC naturally occurring polynucleotide sequence at least 90 % identical to
 CC the polynucleotide sequence, a polynucleotide complementary to them or an
 CC RNA equivalent of them. The polypeptide or polynucleotide are useful for
 CC treating, preventing or diagnosing a disease or condition associated with
 CC the expression of functional SPM. These are particularly useful for
 CC diagnosing, treating or preventing autoimmune/inflammatory disorders
 CC (e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's
 CC disease), neurological disorders (e.g. epilepsy, Huntington's disease,
 CC dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease,
 CC multiple sclerosis, cerebral palsy, Parkinson's disease, anxiety,
 CC schizophrenia or amnesia), or cell proliferative disorders (e.g.
 CC psoriasis, polycythemia vera, or cancers including adenocarcinoma,
 CC leukaemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the brain,
 CC breast, cervix or prostate).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

Sequence 1334 BP; 299 A; 381 C; 394 G; 260 T; 0 other;

Query Match 56.7%; Score 749; DB 25; Length 1334;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 799; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

OY 522 CGGAGCTGAGATTGTTTCAGATCATCATCATGTTGGTGTGATGATGTTGGTGGT 581
DB 105 CGGAGCTGAGATTGTTTCAGATCATCATCATGTTGGTGTGATGATGTTGGTGGT 164
OY 582 TGATCAGCTGCTCTGAGCAGTACAGAGCTGTCTGACAGGTCTTTCATACAGCCGAC 641
DB 165 TGATCAGCTGCTCTGAGCAGTACAGAGCTGTCTGACAGGTCTTTCATACAGCCGAC 224
OY 642 GCCAGGGGGGAGAGAGAAATGCTCTGAGAGAGTGGTGGTGGTGGTGGTGGTGG 701
DB 225 GCCAGGGGGGAGAGAGAAATGCTCTGAGAGAGTGGTGGTGGTGGTGGTGGTGG 284
OY 702 GCACAGTGTACAGAGAAATGCTCTGAGAGAGTGTACAGCCGCTGAGCCACAG 761
DB 285 GCACAGTGTACAGAGAAATGCTCTGAGAGAGTGTACAGCCGCTGAGCCACAG 344
OY 762 ACCGCTGCGCGCTGCGCCCTTCCGCGAGCGGAGCGCTTCCAGCCGCTTCCAGCC 821
DB 345 ACCGCTGCGCGCTGCGCCCTTCCGCGAGCGGAGCGCTTCCAGCCGCTTCCAGCC 404
OY 822 ATCCGTACCTGACAGACAGATTCAGACCTCCACCCACCATCTCGCTTCAGACGGGGAG 881
DB 405 ATCCGTACCTGACAGACAGATTCAGACCTCCACCCACCATCTCGCTTCAGACGGGGAG 464
OY 882 AGCCCCACCTTACAGAGGGCCCTTCCAGACCTTCCAGAGAGAGAGAGAGAGAGAG 941
DB 465 AGCCCCACCTTACAGAGGGCCCTTCCAGACCTTCCAGAGAGAGAGAGAGAGAGAG 524
OY 942 AACTGAACCGGAGAGTGTGCGCGACCCCAAAACAGAACATCTTTCAGACAGTGA 1001
DB 525 AACTGAACCGGAGAGTGTGCGCGACCCCAAAACAGAACATCTTTCAGACAGTGA 584
OY 1002 TGGATAGTGCAGAGTGTGCGCGCCCTTCCAGACCTTCCAGAGAGAGAGAGAGAG 1061
DB 585 TGGATAGTGCAGAGTGTGCGCGCCCTTCCAGACCTTCCAGAGAGAGAGAGAGAGAG 644
OY 1062 CGTGTACAGGAGCGGGGCGCATGAGAGGGCGCGCCCACTTACAGCGAGGATTCG 1121
DB 645 CGTGTACAGGAGCGGGGCGCATGAGAGGGCGCGCCCACTTACAGCGAGGATTCG 704
OY 1122 GCCATACCCGGGGGTCTCTTCCAGACAGCAGAGAGAGAGTGTGCGCGCCCTTCTTGG 1181
DB 705 GCCATACCCGGGGGTCTCTTCCAGACAGCAGAGAGAGAGTGTGCGCGCCCTTCTTGG 764
OY 1182 AGGGAGCCGGGTCTCCACACACACATCGCGCCCTTACAGAGAGCCAGCATCTTGAGCA 1241

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DB 765 AGGGAGCCCGGCTCCACCACACACATCGGCCCTAGAGAGCGCAGCCATCTGAGCA 824
OY 1242 AAGAGAAGGATTAACAGAAAGACACCCTCTCTAGAGGTCCCGAGGGGCGCGCTGAGG 1301
DB 825 AAGAGAAGGATTAACAGAAAGACACCCTCTCTAGAGGTCCCGAGGGGCGCGCTGAGG 884
OY 1302 CTGCGTAGGTGAAAGAGCG 1321
DB 885 CTGCGTAGGTGAAAGAGCG 904

RESULT 7
AAA75163
ID AAA75163 standard; cDNA; 969 BP.
AC AAA75163;
DT 15-JAN-2001 (first entry)
DE cDNA clone encoding a human TANGO 261 polypeptide.
XX
XX TANGO 261; TANGO 261; TANGO 262; TANGO 267;
XX cellular proliferation; cellular differentiation; cellular adhesion;
XX von Willebrand factor-associated disorder; cell trafficking; cancer;
XX hematopoietic associated disease; atelectasis; pulmonary congestion;
XX oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
XX intestinal disorder; spleen associated disease; renal disorder;
XX cardiovascular disorder; ischemic heart disease; hydrocephalus;
XX brain herniation; latrogenic disease; inflammation; meningitis;
XX Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;
XX multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 6..764
XX FT /*tag= a
XX FT /product= "TANGO 261"
XX
XX WO200052022-A1.
XX
XX 08-SEP-2000.
XX
XX 01-MAR-2000; 2000WO-US05226.
XX
XX 01-MAR-1999; 99US-0122458.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Barnes TM, Holtzman DA, Sharp JD, Fraser CC;
XX
XX WPI: 2000-579269/54.
XX P-PSDB: AAB18461.
XX
XX Novel human and murine secreted proteins designated TANGO 216, 261,
XX 262, 266 and 267 useful as modulating agents of cellular processes,
XX e.g. for treating cancer -
XX
XX PS Disclosure: Page -; 175pp; English.
XX
XX AAA75163-65 encode human TANGO 261 proteins. The specification also
XX describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO
XX polypeptides can be used to modulate cellular proliferation, modulate
XX cellular differentiation and/or modulate cellular adhesion. The
XX proteins can be used to treat any von Willebrand factor-associated
XX disorder, regulate extracellular matrix structuring, cellular adhesion,
XX and cell trafficking and/or migration, modulate cellular interactions,
XX modulate cell adhesion in proliferative disorders, such as cancer,
XX modulate the proliferation, differentiation, and/or function of cells
XX that appear in the bone marrow, and leukocytes, treat bone marrow, blood
XX and hematopoietic associated diseases and disorders, atelectasis,
XX pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial
XX asthma and bronchiectasis, intestinal disorders, spleen associated

```

db 795 TAGGTGAAAGGCAG 809

CC hydrocephalus and encephalitis, and treat hepatic disorders.

QY 1090 GGGGCCCCCCCCCTACAGGAGGTCATGGCCACTACCCGGGGTCTCTTCACGA 1149
| | | | |
DB 1187 GGGGCGCGCCGACCTACAGGAGTATCGGCGCCTACCCGGGGTCTCTTCACGA 1246
| | | | |
QY 1150 CCAGAGAGCACTGGGGCGCCCTCTCTGAGGGGACCCGGCTCCACACACACAT 1209
| | | | |
DB 1247 CCAGAGAGCACTGGGGCGCCCTCTCTGAGGGGACCCGGCTCCACACACAT 1306
| | | | |
QY 1210 GCGGCCCCCTAGAGAGCGAGCATCTGAGGAGGAGGATTAAGAGAGAGAGAGAG 1269
| | | | |
DB 1307 GCGGCCCCCTAGAGAGCGAGCATCTGAGGAGGAGGATTAAGAGAGAGAGAGAG 1366
| | | | |
QY 1270 TCTTAGGGTCCCGCAGGGG 1289
| | | | |
DB 1367 TCTTAGGGTCCCGCAGGGG 1386
| | | | |

RESULT 11
AAf65983 standard; cDNA; 408 BP.
AAf65983;
AAf65983;
09-APR-2001 (first entry)
Novel human polynucleotide, SEQ ID NO: 1739.
Human; cytosolic; gene therapy; colon cancer; prostate cancer;
breast cancer; lung cancer; cancer detection; ss.
Homo sapiens.
WO200102568-A2.
11-JAN-2001.
30-JUN-2000; 2000WO-US18374.
02-JUL-1999; 99US-0142310.
02-JUL-1999; 99US-0142311.
(CHIR) CHIRON CORP.
(HYSE-) HYSEQ INC.
Williams LT, Escobedo J, Innis MA, Garcia PD, Klinger J, Kassam A;
Reinhard C, Randazzo F, Kennedy GC, Pot D, Lamson G, Drmanac R;
Cirenjakov R, Drmanac S, Dickson M, Labat I, Leshowitz D;
Kita D, Garcia V, Jones LM, Strache-Crain B;
WPI; 2001-091805/10.

Library of polynucleotides for diagnosing a cancerous state of a
mammalian cell and detecting cancer, particularly of the colon or
prostate, comprises 3351 human polynucleotide sequences -
Claim 9; Page 793; 1046bp; English.

The present sequence is one of 3351 sequences in a library of human
polynucleotides. The library is used to detect differentially expressed
genes correlated with a cancerous state of a mammalian cell and can
detect colon, prostate, breast and lung cancer. The library can be used
to produce probes for detection of mRNA and to produce additional copies
of the polynucleotides. The probes can be used for chromosome mapping of
the polynucleotide and for detection of transcription levels. Ribozymes
or antisense oligonucleotides can be generated. The polynucleotides and
their gene products are used as genetic or biochemical markers (e.g. in
blood or tissues) that will detect the earliest changes along the
carcinogenesis pathway and/or monitor the efficacy of therapies and
preventive interventions. The polynucleotides, polypeptides and
antibodies against them can be used in pharmaceutical compositions to
treat the cancers and proliferative disorders such as neoplasia,
dysplasia and hyperplasia.

XX SQ Sequence 408 BP; 81 A; 159 C; 115 G; 53 T; 0 other;
Query Match 30.4%; Score 401; DB 22; Length 408;
Best Local Similarity 100.0%; Pred. No. 4,1e-170;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 583 GATCAGTGCCTGCTGAGGCACTACAAAGTGTCTGACAGGCTTCATCAGCGGACAG 642
| | | | |
DB 8 GATCAGTGCCTGCTGAGGCACTACAAAGTGTCTGACAGGCTTCATCAGCGGACAG 67
| | | | |
QY 643 CCAGGGGCGGAGAGAGAGATGCTGTCTCAGAGAGATGCTGTGCTCGGAGAG 702
| | | | |
DB 68 CCAGGGGCGGAGAGAGAGATGCTGTCTCAGAGAGATGCTGTGCTCGGAGAG 127
| | | | |
QY 703 CACAGTGTGAGGCAAGAGATCCAGAGGCGGAGGCTCTGAGGCGGCGGCGGAGAG 762
| | | | |
DB 128 CACAGTGTGAGGCAAGAGATCCAGAGGCGGAGGCTCTGAGGCGGCGGAGAG 187
| | | | |
QY 763 CCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 822
| | | | |
DB 188 CCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 247
| | | | |
QY 823 TCCGTACCTGACAGCAGAGATGAGCTGCTGACCATCTGCTGTGAGAGGAGAG 882
| | | | |
DB 248 TCCGTACCTGACAGCAGAGATGAGCTGCTGACCATCTGCTGTGAGAGGAGAG 307
| | | | |
QY 883 GCCCCACCTACAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 942
| | | | |
DB 308 GCCCCACCTACAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 367
| | | | |

QY 943 ACTGAACCGGAGATGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 983
| | | | |
DB 368 ACTGAACCGGAGATGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 408
| | | | |

RESULT 12
AAI59654/c
AAI59654 standard; cDNA; 1069 BP.
AAI59654;
AAI59654;
22-OCT-2001 (first entry)
Human polynucleotide SEQ ID NO 3643.
DE Human polynucleotide; cytosolic; gene therapy; cancer;
XX Human; neurotropic; immunosuppressant; neurotropic; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemofactis;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
leukemia; ss.
XX
OS Homo sapiens.
XX
XX WO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US34263.
XX
XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-0552317.
XX 09-JUL-2000; 2000US-0598042.
XX 19-JUL-2000; 2000US-0620312.
XX 03-ANG-2000; 2000US-0653450.
XX 14-SEP-2000; 2000US-0662191.
XX 19-OCT-2000; 2000US-0693036.
XX 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI

XX
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.

xx Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E,
pi

XX WPI; 1999-621386/54
DR 1999-621386/54

DR WPI; 1999-021300/54.
DR P-PSDB; MAY74135, MAY74136, MAY74137.
DR

XX New human nucleic acid sequences from pancreatic tumors, and related
PT proteins -
PT

XX
PS Claim 2; Page 269-270; 502pp; German.

XX This invention describes novel polypeptides and their encoding nucleic acids derived from human pancreatic tumor tissue which have cytotoxic activity. The sequences are also useful in producing pharmaceutical compositions for treatment of pancreatic tumors. AA52858-25014 CC represent expressed sequence tag (EST) fragments derived from a human pancreatic tumor cDNA library and which encode the proteins represented in AA573814-Y74252.

Sequence 812 BP; 157 A; 272 C; 237 G; 146 T; 0 other;

Query Match	20.5%;	Score 271;	DB 20;	Length 812;
Best Local Similarity	99.7%;	Pred. No. 9.6e-112;		
Matches 321;	Conservative	0;	Mismatches 1;	Indels 0;
				Caps 0

QY	585	TCACGTGCTCGTGTGAGCCACTACAGCTGTGTGCACGGCTCTTCAACGACGGGCAAGCC	644
Db	426	TCACGTGCTCGTGTGAGCCACTACAGCTGTGTGCACGGCTCTTCAACGACGGGCAAGCC	485
QY	645	AGGGGGGAGAGAGAGAGATGCTCTGTCTCAGAAAGATGCTGTGCTCTCGAAGACA	704
Db	486	AGGGGGGAGAGAGAGAGATGCTCTGTCTCAGAAAGATGCTGTGCTCTCGAAGACA	545
QY	705	CAGTGTACAGGCACAAAGGAATCCGAGAGCGGACAGGTCTACGGCCCGCTCTGGGCCACCGACC	764
Db	546	CAGTGTACAGGCACAAAGGAATCCGAGAGCGGACAGGTCTACGGCCCGCTCTGGGCCACCGACC	605
QY	765	GCGTGGGCGGTGCCGCCCTTGCGCCACGGGAGCGCTTTCACAGCGTTCACAGGCCACCTATTC	824
Db	606	GCGTGGGCGGTGCCGCCCTTGCGCCACGGGAGCGCTTTCACAGCGTTCACAGGCCACCTATTC	665
QY	825	CGTACCGGACGACAGAGATCGACTTGCACACCACCAATCTCGCTGTACAGCGGGAGAGAC	884
Db	666	CGTACCGGACGACAGAGATCGACTTGCACACCACCAATCTCGCTGTACAGCGGGAGAGAC	725
	885	CCCCACCTTACAGAGGCGCCCTG	906
	726	CCCCACCTTACAGAGGCGCCCTG	747

Search completed: August 27, 2003, 21:42:01
Job time : 421 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 27, 2003, 21:24:48 ; Search time 3109 Seconds

(Without alignments)
10326.862 Million cell updates/sec

Title: US-09-934-249-1

Perfect score: 1321

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Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 44005525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:
1: em_estbta:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_huv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mus:*
23: em_gss_mam:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrt1:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1.	632	47.8	1046	12	BM922276 AGENCOURT
2	614	46.5	967	13	BM641849 AGENCOURT
3	568	43.0	916	13	BM954555 AGENCOURT
4	558	42.2	609	13	BM636742 hdl3h06.y

5	550	41.6	551	12	BM141979
6	538	40.3	951	13	AL558881
7	518	39.2	729	13	BM575741
8	511	38.7	850	13	BM602918
9	497	37.6	890	13	BM690750
10	471	35.7	1068	13	BM527705
11	468	34.1	655	13	BM691705
12	450	34.0	945	13	BM859860
13	449	33.7	782	12	BM053219
14	445	33.5	602	14	CA431191
15	442	33.4	661	12	BM712680
16	441	33.1	633	13	BM714472
17	437	32.4	588	13	BM624784
18	428	32.4	1007	9	AL558882
19	425	32.2	1201	9	AL517150
20	424	32.1	844	13	BM686793
21	422	31.9	938	13	BM157842
22	422	31.9	952	13	BM157959
23	422	31.9	1280	13	BM691500
24	422	31.9	1280	13	BM691500
25	417	31.6	559	10	BE855409
26	417	31.6	629	13	BM730650
27	406	30.7	1400	12	BM559329
28	401	30.4	730	12	BM677602
29	399	30.2	626	12	BM974296
30	393	29.8	728	13	BM683523
31	390	29.5	973	13	BM169156
32	383	29.0	570	13	BM575582
33	377	28.5	563	12	CB048800
34	365	27.6	552	12	BM713900
35	358	27.1	1127	13	BM174654
36	348	26.3	646	13	BM859841
37	338	25.6	874	13	BM362396
38	331	25.1	899	13	BM196912
39	327	24.8	547	12	BM676516
40	324	24.5	613	10	BM680325
41	302	22.9	651	14	CB554226
42	302	22.9	593	9	AI761441
43	291	22.0	602	9	AI921394
44	288	21.8	668	14	CB044866
45	286	21.7	446	12	BM681946

ALIGNMENTS

RESULT 1
BM922276 1046 bp mRNA linear EST 12-MAR-2002
AGENCOURT_6707077 NIH_MGC_115 Homo sapiens CDNA clone IMAGE:5754437
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BM922276.1 GI:19372655
EST.
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NIH-MGC http://mhc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgepds-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM12791 row: n column: 06
High quality sequence stop: 671.

Db	Accession	LOCUS	DEFINITION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Db	241	CGCCTGGGCGCGCCGCTTCGCCAGGAGGCGCTTCACCGCTTCACCGCACCTAT								
Oy	824	CCGTAACCTGGAGACAGAGATGTGACCTGGCACCCACACATCTGCTGTACAGAGGGAGAG								
Db	301	CCGTAACCTGGAGACAGAGATGTGACCTGGCACCCACACATCTGCTGTGTACAGAGGGAGAG								
Oy	884	CCCCCACCCTTACACAGAGGGCCCTTGCACACCTCCAGCTTGGGAGACCCCGAGACACACTGGAA								
Db	361	CCCCCACCCTTACACAGAGGGCCCTTGCACACCTCCAGCTTGGGAGACCCCGAGAGACACTGGAA								
Oy	944	CTGAACCGGGAGGTGGGTGTGGCGGCACACCCCAAACAGAACCATCTTGACAGTGTGACTGATG								
Db	421	CTGAACCGGGAGGTGGGTGTGGCGGCACACCCCAAACAGAACCATCTTGACAGTGTGACTGATG								
Oy	1004	GATAGTGCCAGAGCTGGGGCGGCGCCCTTGCCACACAGAGAGAGAGTGGGCGCCCTCTGTGTGAG								
Db	481	GATAGTGCCAGAGCTGGGGCGGCGCCCTTGCCACACAGAGAGAGAGTGGGCGCCCTCTGTGTGAG								
Oy	1124	CACATACCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG								
Db	601	CACATACCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG								
Oy	1184	GGGAGCCGCGGCTTCACACACACACATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG								
Db	661	GGGAGCCGCGGCTTCACACACACACATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG								
RESULT 3										
LOCUS	B0954555									
DEFINITION	AGENCOURT_8825282 lupsk1.sc1atic.nerve Homo sapiens cDNA clone									
KEYWORDS	B0954555									
ACCESSION	B0954555.1									
VERSION	GI:22370033									
EST										
ORGANISM	Homo sapiens (human)									
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.									
TITLE	1 (bases 1 to 916)									
JOURNAL	NIH-MGC HtLP://mhc.nci.nih.gov/.									
COMMENT	Unpublished Contact: Robert Strausberg, Ph.D. Email: rgsrbs@mail.nih.gov Tissue Procurement: Dr. James R. Lupski cDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLNL3626 row: C column: 10 High quality sequence stop: 669. Location/Qualifiers 1. 916 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6204609" /sex="male" /tissue_type="sciatic nerve" /dev_stage="adult, 70 yr" /lab_host="DH10B" /clone_id="lupsk1.sc1atic.nerve" /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1: Nottl, Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors:									

Query Match	Best Local Similarity	Score	DB 13:	Length	916:
Matches	668:	Conservative	0:	Mismatches	2:
				Indels	0:
				Gaps	0:
OY	344	GC	GC	GC	GC
DB	1	GC	GC	GC	GC
OY	404	GC	GC	GC	GC
DB	61	GC	GC	GC	GC
OY	464	CC	CC	CC	CC
DB	121	CC	CC	CC	CC
OY	524	GAG	GAG	GAG	GAG
DB	181	GAG	GAG	GAG	GAG
OY	584	ATC	ATC	ATC	ATC
DB	241	ATC	ATC	ATC	ATC
OY	644	CAG	CAG	CAG	CAG
DB	301	CAG	CAG	CAG	CAG
OY	704	ACA	ACA	ACA	ACA
DB	361	ACA	ACA	ACA	ACA
OY	764	GCG	GCG	GCG	GCG
DB	421	GCG	GCG	GCG	GCG
OY	824	CGT	CGT	CGT	CGT
DB	481	CGT	CGT	CGT	CGT
OY	884	CCC	CCC	CCC	CCC
DB	541	CCC	CCC	CCC	CCC
OY	944	CTG	CTG	CTG	CTG
DB	601	CTG	CTG	CTG	CTG
OY	1004	GAT	GAT	GAT	GAT
DB	661	GAT	GAT	GAT	GAT

BASE COUNT 162 a 354 c 273 g 127 t

ORIGIN

Query Match 43.0% Score 568; DB 13: Length 916;

Best Local Similarity 99.7%: Pred. No. 4.3e-241;

Matches 668: Conservative 0: Mismatches 2: Indels 0: Gaps 0:

5'-GACATCCCGGCGTCCG-3' and
5'-GACATGCTGATGATGCGGCGGCGGCGGCTT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupszki, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies.*

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (pages 1 to 609)
Mistow, G., Bernstein, S.L., Wyatt, M.K., Ray, S., Behal, A., Touchman, A., Bouffard, G., Smith, D. and Peterson, K.
Expressed sequence tag analysis of human retina for the NEIRBank Project: Rebinding, an abundant, novel retinal cDNA and alternative splicing of other retina-preferred gene transcripts
Mol. Vis. 8 (4), (2002) In press
Contact: Mistow, G.
Section: Neurobiology: Structure and Function

6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: grame@helix.nih.gov
Plate: 13 row: h column: 06
Seq primer: M13P1 reverse primer (ABI).
Location/Qualifiers
1..609
source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="hd1306"
/tissue_type="Retina"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_1kb="Human Retina cDNA (Un-normalized, unamplified
): hd/be"
)/note="Organ: Eye; Vector: pSPOR1; Neural retina tissue
was dissected from two 80 year old donors with no observ
eye disease. 100ug of total RNA was used for library
construction. A directionally cloned cDNA library in the
pSPOR1 vector (Life Technologies) was constructed at
Bioserve Biotechnology (Laurel MD) essentially followin
the protocols of the Superscript Plasmid System full
details of which are contained in the manufacturer's
instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
primer-adaptor [5'-gcagctactctgagtcgacgccgcc\(T\)]-5'-
analyses was performed on the unamplified library
at the NIH Intramural Sequencing Center (NISC)."

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Query Match	42.2%	Score 558	DB 13	Length 609
Best Local Similarity	99.8%	Pred. No. 1.2e-236		
Matches	608	Conservative	0	Mismatches 1
			Indels	0
			Gaps	
Db	631	CAGCCGGCACAGCCAGGGGGGGGAGAGAGAAAGATGCCCTGTCTTCAGAGAGATCCCTGTG	6	
	1	CAGCCGGCACAGCCAGGGGGGGGAGAGAGAAAGATGCCCTGTCTTCAGAGAGATCCCTGTG	6	
QY	691	GCCTTCGGAGAGACAGTGTTCAGGCACACGAAATCCAGAGCCGAGAGGTCTACGGCCGGCC	7	
Db	61	GCCTTCGGAGAGACACAGTGTTCAGGCACACGAAATCCAGAGCCGAGAGGTCTACGGCCGGCC	1	
QY	751	TCGGCCCAACACAGCCGCTTGCCGTCGCGCCCTTTCAGCCAGCGGGAGGCGTTCACACGCTT	8	
Db	121	TCGGCCCAACACAGCCGCTTGCCGTCGCGCCCTTTCAGCCAGCGGGAGGCGTTCACACGCTT	1	
QY	811	CCAGCCCAACCTATCCGTACCTGCAGACAGAGATGACCTGCGACACCAACATCTTCGCTGC	8	
Db	181	CCAGCCCAACCTATCCGTACCTGCAGACAGAGATGACCTGCGACACCAACATCTTCGCTGC	2	
QY	871	AGACGGGGAGAGAGCCCCACCCCTACACAGGCGCCCTGCACCTCCAGCTTGGGGACCCCGA	9	
Db	241	AGACGGGGAGAGAGCCCCACCCCTACACAGGCGCCCTGCACCTCCAGCTTGGGGACCCCGA	3	
QY	931	GCAGAGCTGGAACCTGAACCGGGAGTGGGTGGGGACACCCCAACAGAAACATCTTCGA	9	
Db	301	GCAGAGCTGGAACCTGAACCGGGAGTGGGTGGGGACACCCCAACAGAAACATCTTCGA	3	

QY	991	CAGTACGACTGATGATAGTATAGTGCACAGGCTGGGGGGGCGCCCTTGCCGCCCCACAGCACTAATCTGGG	1050
Db	361	CAGTACGACTGATGATAGTATAGTGCACAGGCTGGGGGGGCGCCCTTGCCGCCCCACAGCACTAATCTGGG	420
QY	1051	CATATAGGCGCCACGCGCTATACGGGCACGGCGGGGCGCATGGAGGGGGGCGCGCGCCACTTACAG	1110
Db	421	CATATAGGCGCCACGCGCTATACGGGCACGGCGGGGCGCATGGAGGGGGCGCGCGCCACTTACAG	480
QY	1111	CGAGGTCATCGGCACACTACCCGGGGTCTCTCTTCCAGCACCCAGCAGAGACAGTGGGGCGCC	1170
Db	481	CGAGGTCATCGGCACACTACCCGGGGTCTCTCTTCCAGCACCCAGCAGAGACAGTGGGGCGCC	540
QY	1171	CTCCTTGCTGGAGGGGACCGGGCGTCCACCAACACATCGCGGGCCCTAGAGAGCGAGC	1230
Db	541	CTCCTTGCTGGAGGGGACCGGGCGTCCACCAACACATCGCGGGCCCTAGAGAGCGAGC	600
QY	1231	CATCTGGAG 1239	
Db	601	CATCTGGAG 609	

LOCUS	BM141979	551 bp	mRNA	linear	EST 12-MAR-2002
DEFINITION	1f52a11.y1 Melton Normalised Human Islet 4 N4-HIS 1 Homo sapiens				
	cdna IMAGE:5677341 5' similar to TR:Q9UUD3 Q9UUD3 DJ718J7.1				
	;; mRNA sequence.				

ACCESSION	BM41979	GI:17152046
VERSION	BM41979.1	
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

REFERENCE	AUTHORS
1 (bases 1 to 551)	Kent, G., Permutt, A., Lee, C., Kaestner, K., Melton, D., Brown, J.,
	Eukaryota; Metazoa; Chordata; Euthalia; Primates; Catarrhini; Homnidae; Homo;
	Craniata; Vertebrata; Euteleostomi;

TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished
COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@molb.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brownjfas.harvard.edu) This sequence now available from the IMAGE
consortium, for clone orders contact: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 429.

Location/Qualifiers
1..551

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image:5677341"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/clone_lib="Wellton Normalized Human Islet 4 N4-HIS 1"
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
SuperScript plasmid library kit (Life Technologies). cDNA
made by oligo-dT priming. Size selected by column

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Db 306 ACTACCGGGGCTCTCTCCACACACAGACAGAGTGGGCGCCCTCTCTCTGAGG 247
QY 1185 GGAACCGGCTCCACACACACATGCGCCCTTAGAGAGCGACCATCTGGAGCAAG 1244
Db 246 GGAACCGGCTCCACACACACATGCGCCCTTAGAGAGCGACCATCTGGAGCAAG 187
QY 1245 AGAAGATTAACAGAAAGACACCCCTCTCTAGAGTCCCGAGGGGGCGGCTGGGGCG 1304
Db 186 AGAAGATTAACAGAAAGACACCCCTCTCTAGAGTCCCGAGGGGGCGGCTGGGGCG 127
QY 1305 CGTAGGTGAAGAGCAG 1321
Db 126 CGTAGGTGAAGAGCAG 110

RESULT 7
B0575741/c 729 bp mRNA linear EST 19-JUN-2002
LOCUS B0575741
DEFINITION UT-H-E21-bdg-h-14-0-UT.s1 NCI-CGAP Ch2 Homo sapiens cDNA clone
UT-H-E21-bdg-h-14-0-UT 3', mRNA sequence.

ACCESSION B0575741 GI:21479058
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 729)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
Orthopedics

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES

Source

1. 729
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UT-H-E21-bdg-h-14-0-UT"
/tissue_type="Chondrosarcoma Grade II"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_id="NCI-CGAP Ch2"
/note="Organ: Left Pelvis; Vector: pRT3-Pac (Pharmacia)
With a modified polylinker. Site_1: EcoR I, Site_2: Not I.
NCI-CGAP Ch2 is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma Grade II. The library
was constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pRT3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
TGATACGCT
TAG-LIB-UT-H-E21
TAG-TISSUE-grade-2-chondrosarcoma
TAG_SEQ-ATCTAATATG"
BASE COUNT 101 a 213 c 253 g 162 t
ORIGIN

Query Match 39.2%; Score 518; DB 13; Length 729;
Best Local Similarity 99.8%; Pred. No. 6-6e-219;
Matches 368; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 753 GGCACACGACGCGCTGGGCGCTGCGCCCTTGCCAGCGGAGCGCTTCCACCGCTTCC 812
Db 729 GGCACACGACGCGCTGGGCGCTGCGCCCTTGCCAGCGGAGCGCTTCCACCGCTTCC 670
QY 813 AGCCCACTATCCGATACCTGCGAGCAAGATGATGATGATGATGATGATGATGATGAT 872
Db 669 AGCCCACTATCCGATACCTGCGAGCAAGATGATGATGATGATGATGATGATGATGAT 610
QY 873 AGCGGAGAGAGCGCCCGACCCCTACAGAGGCGCCCTGACACCTCCAGCTTGGAGCCCGAGC 932
Db 609 AGCGGAGAGAGCGCCCGACCCCTACAGAGGCGCCCTGACACCTCCAGCTTGGAGCCCGAGC 550
QY 933 AGCAGCTGAGACTGAACCGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 992
Db 549 AGCAGCTGAGACTGAACCGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 490
QY 993 GTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1052
Db 489 GTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 430
QY 1053 TCAGCGCCACAGTGTCTACAGGCGGCGGCGCATGGAGGGCGCCCGCCACCTACAGCG 1112
Db 429 TCAGCGCCACAGTGTCTACAGGCGGCGGCGCATGGAGGGCGCCCGCCACCTACAGCG 370
QY 1113 AGGTCACTGGGCGACCTACCGGGGCTCTCTCTCCAGCAGCAGCAGCAGCAGCAGCAGC 1172
Db 369 AGGTCACTGGGCGACCTACCGGGGCTCTCTCTCCAGCAGCAGCAGCAGCAGCAGCAGC 310
QY 1173 CCTTGTGAGGAGGAGCGGCTCTCCACACACACATGCGCCCTTAGAGCGCAGCCA 1232
Db 309 CCTTGTGAGGAGGAGCGGCTCTCCACACACACATGCGCCCTTAGAGCGCAGCCA 250
QY 1233 TCTGAGCAAAAGAGAGATTAACAGAAAGAGACCTCTCTAGAGTCCCGAGGGGGCC 1292
Db 249 TCTGAGCAAAAGAGAGATTAACAGAAAGAGACCTCTCTAGAGTCCCGAGGGGGCC 190
QY 1293 GGGCTGGGCGCTGCTAGTGAAGAGCAG 1321
Db 189 GGGCTGGGCGCTGCTAGTGAAGAGCAG 161

RESULT 8
B0602918 850 bp mRNA linear EST 20-SEP-2002
LOCUS B0602918
DEFINITION AGENCOURT.10016502 NIH-MGC.142 Homo sapiens cDNA clone
IMAGE:6497853 5', mRNA sequence.

ACCESSION B0602918 GI:23254677
VERSION B0602918
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 850)
NIH-MGC <http://mhc.ncbi.nlm.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-remail.nih.gov
Tissue Procurement: NCI

cDNA Library Preparation: Michael Brownstein Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: L10M2679 row: 1 column: 22
High quality sequence stop: 499.
Location/Qualifiers

FEATURES

QY 822 ATCCGTAAGTGCAGCAGAGATCGACCTGCGCCACCCACCATCTGCTGACAGAGGGAGG 881
 DB 428 ATCCGTAAGTGCAGCAGAGATCGACCTGCGCCACCCACCATCTGCTGACAGAGGGAGG 487
 QY 882 AGCCCCCAGCTTACAGAGGGGCCCCCTGACACCTTCCAGCTTGGGGAGCCCCAGACAGCTGCG 941
 DB 488 AGCCCCCAGCTTACAGAGGGGCCCCCTGACACCTTCCAGCTTGGGGAGCCCCAGACAGCTGCG 547
 QY 942 AACTGAACCGGAGAGTGTGCGCGCACCCCAACAAACATCTTGCAGAGTGA 1001
 DB 548 AACTGAACCGGAGAGTGTGCGCGCACCCCAACAAACATCTTGCAGAGTGA 607
 QY 1002 TGGATAGTGCAGAGCTGGGGCGGCCCCCTGCGCCACCCAGAGTGA 1061
 DB 608 TGGATAGTGCAGAGCTGGGGCGGCCCCCTGCGCCACCCAGAGTGA 667
 QY 1062 CGTGTAC 1069
 668 CGTGTAC 675

RESULT 10
 LOCUS B0527705 1068 bp mRNA linear EST 13-SEP-2002
 DEFINITION AGENCOURT_10186171 NIH_MGC_101 Homo sapiens cDNA clone
 IMAGE:6537543 5', mRNA sequence.
 ACCESSION B0527705
 VERSION B0527705.1 GI:22838146
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 TITLE NIH-MGC http://mgi.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA library Preparation: Rubin Laboratory
 CDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LCM2700 row: k column: 15
 High quality sequence stop: 468.
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:6537543"
 /tissue_type="epidermoid carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_101"
 /note="Organ: Lung; Vector: pOTB7; Site:1: EcoRI; Site:2:
 XhoI; cDNA made by oligo-dt priming, directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC library"

BASE COUNT 154 a 445 c 330 g 135 t 4 others
 ORIGIN

Query Match 35.7%; Score 471; DB 13; Length 1068;
 Best Local Similarity 100.0%; Pred. No. 4.5e-198;
 Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 GGGAAAGCTAGCGGAGAGGCTCAGCCCGCGGAGCGCGCCCGCTGCCAGCCCAT 151
 DB 21 GGGAAAGCTAGCGGAGAGGCTCAGCCCGCGGAGCGCGCCCGCTGCCAGCCCAT 80
 QY 152 TTTCGGAGAGCCACCGCGGGGCACTGCCAGAGCCCCGGGGGTGCGGAGGGAGCGCGG 211
 DB 81 TTTCGGAGAGCCACCGCGGGGCACTGCCAGAGCCCCGGGGGTGCGGAGGGAGCGCGG 140
 QY 212 GGGGCGAGCGGAGAGCGGCTCCCGGACACTGAGACCCCGCGGAGCCCGGGAACTTGACGG 271
 DB 141 GGGGCGAGCGGAGAGCGGCTCCCGGACACTGAGACCCCGCGGAGCCCGGGAACTTGACGG 200
 QY 272 CGACCCGAGCGCGGAGAGCGGCGGCGGCTCCCGCGGAGCGGCTCTGACATGCGGGG 331
 DB 201 CGACCCGAGCGCGGAGAGCGGCGGCGGCTCCCGCGGAGCGGCTCTGACATGCGGGG 260
 QY 332 CCGCAGCTCCGGGCGCGCGGAGAGCCCGCGGAGCGGCGGCGGCGGCGGCGGCGG 391
 DB 261 CCGCAGCTCCGGGCGCGCGGAGAGCCCGCGGAGCGGCGGCGGCGGCGGCGGCGG 320
 QY 392 CGCGGCGGCGCGCGGCGGCTCCATGACACCGCTTGTGAGGGGTCAACAGACCGCGGCGG 451
 DB 321 CGCGGCGGCGCGCGGCGGCTCCATGACACCGCTTGTGAGGGGTCAACAGACCGCGGCGG 380
 QY 452 GCGCGCGGCGGAGCCCAATGCTCTGACAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 511
 DB 381 GCGCGGCGGAGCCCAATGCTCTGACAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 440
 QY 512 ATGAGATCAGGAGGTGAGTGTTCAGATCATCATCATCATCATCATCATCATCATCATCAT 562
 DB 441 ATGAGATCAGGAGGTGAGTGTTCAGATCATCATCATCATCATCATCATCATCATCATCAT 491

RESULT 11
 LOCUS B0691705 655 bp mRNA linear EST 15-JUL-2002
 DEFINITION AGENCOURT_8046876 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6208939
 IMAGE:6537543 5', mRNA sequence.
 ACCESSION B0691705
 VERSION B0691705.1 GI:21817021
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 JOURNAL NIH-MGC http://mgi.nci.nih.gov/
 COMMENT Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA library Preparation: Rubin Laboratory
 CDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LCM2367 row: g column: 20
 High quality sequence stop: 645.
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6208939"
 /tissue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pOTB7; Site:1: XhoI;
 Site:2: EcoRI; cDNA made by oligo-dt priming,
 directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed by

QY	875	GGGAGAGAGCCCAACCTTACAGAGGCCCTGCACACCTTCAGCTTCGGAGACCCCGACG	934
Db	605	GGNAGAGAGCCCCACACCTTACCAGAGGCCCTTCGACACCTTCGAGCTTCGAGACCCCGAGCAG	546
QY	935	CAGCTGGAACGTGAACCCGGAGTCCGTGCGGCACACCCCAACAGAACCATCTTGCACAGT	994
Db	545	CAGCTGGGAACGTGAACCCGGAGTCCGTGCGGCACACCCCAACAGAACCATCTTGCACAGT	486
QY	995	GACCTGATGATGATGATGCCAGGCTGGGGGGGCCCTGCCCCCAGAGATTAATCCGGGACATC	105
Db	485	GACCTGATGATGATGATGCCAGGCTGGGGGGGCCCTGCCCCCAGAGATTAATCCGGGACATC	426
QY	1055	AGCCGCACAGTCTACGGCAGCGCGCGCGCGCATGAGAGGGGCCGCGCCACCTACAGCAG	1114
Db	425	AGCCGCACAGTCTACGGCAGCGCGCGCGCGCATGAGAGGGGCCGCGCCACCTACAGCAG	366
QY	1115	GTCATTCGGCCACTACCCCGGGGTCTCTCTCTTCACGACACGACAGAGATGCGGCCCTTCC	1174
Db	365	GTCATTCGGCCACTACCCCGGGGTCTCTCTCTTCACGACACGACAGAGATGCGGCCCTTCC	306
QY	1175	TTGCTGAGAGGGAGCCCGGCTCCACCCACACACATCGCGCCCTTGAAGGCGCAGCCATC	1234
Db	305	TTGCTGAGAGGGAGCCCGGCTCCACCCACACACATCGCGCCCTTGAAGGCGCAGCCATC	246
QY	1235	TGAGACAAAGAGAAAGATAAACAGAGAAAGACACCCCTCTTAGGGTCCCCAGAGGGGGCCGG	1294
Db	245	TGAGACAAAGAGAAAGATAAACAGAGAAAGACACCCCTCTTAGGGTCCCCAGAGGGGGCCGG	186
QY	1295	GCTGGGG 1301	
Db	185	GCTGGGG 179	

RESULT 15
 CA331191/c
 LOCUS
 DEFINITION
 CA331191
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 602)
 NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CCAP).
 Tumor Gene Index
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: James Martin
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 CDNA Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@iowa.edu
 Seq primer: M13 FORWARD
 POLY-a:yes
 Location/Qualifiers
 1.602

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="U1-H-FG1-b91-c-12-0-U1"
/tissue_type="Cell lines"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_idb="NCI CGAP FG1"
/note="Organ: Enchondroma; Vector: pT73-Pac (Pharmacia)
with a modified polylinker Site_1: EcoR I; Site_2: Not I"

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BASE COUNT
ORIGIN

83 a 179 c 196 g 144 t

NCI_CGAP_ENR1 is a normalized cDNA library constructed from a pool of mRNA from 2 cell lines from Enchondroma tissues. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7-3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)₁₈ tail. The sequence tag for this library is CCGTCACATC. The cell lines were from Dr. James Martin from the University of Iowa.

TAG: LIB-UI-H-PG1
TAG: TISSUE-Enchondroma cell line (Mix of EN1 and EN2)
TAG_SEQ:CGGTCTCTC

Query Match	33.5%	Score 442	DB 142	Length 602
Best Local Similarity	100.0%	Pred. No. 3,4e-185		
Matches 442	Conservative 0	Mismatches 0	Indels 0	Gaps 0
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DB	602	GGAGCCCCCACCCTTACACAGGGCCCCCTGCACCTCCAGCTTGGGGACCCCGAGCAGACCT	543	
QY	940	GGAACTGAACCGGGAGTGGTGGCGGACCCCAAGAAACATCTTCGACAGTACCT	999	
DB	542	GGAACTGAACCGGGAGTGGTGGCGGACCCCAAGAAACATCTTCGACAGTACCT	483	
QY	1000	GATGATATGTGCCAGAGCTGGGCGGGCCCTGCCCCCAGCAGTAACTCGGCGATCAGCGC	1055	
DB	482	GATGATATGTGCCAGAGCTGGGCGGGCCCTGCCCCCAGCAGTAACTCGGCGATCAGCGC	423	
QY	1060	CACGGGTCAAGGGGACGGGGGGGGGCGATGGAGGGGGCGGGCCACCTTCAGGAGAGTAT	1119	
DB	422	CACGTGCTACGGCAGCGCGCGGGCGCATGGAGGGGGCGGGCCACCTTCAGGAGAGTAT	363	
QY	1120	CGGCCACTACCCGGGGGCTCTCTTTCAGACACCAGCAGAGCAGTGGGGCGCCCTCTTCTCT	1175	
DB	362	CGGCCACTACCCGGGGGCTCTCTTTCAGACACCAGCAGAGCAGTGGGGCGCCCTCTTCTCT	303	
QY	1180	GGAGGGGACCCGGGCTCCACACACACATGCGGGCCCTTAGAGAGCGAGCATTTGGAG	1233	
DB	302	GGAGGGGACCCGGGCTCCACACACATGCGGGCCCTTAGAGAGCGAGCATTTGGAG	243	
QY	1240	CAAGAGAAAGGATAAACAGAAAGACACCTCTTAAAGGTCCCCAGGGGGGGCGGGCTGG	1299	
DB	242	CAAGAGAAAGGATAAACAGAAAGACACCTCTTAAAGGTCCCCAGGGGGGGCGGGCTGG	183	
QY	1300	GGGTGCGTGAAGTGAAAAAGGAC	1321	
DB	182	GGGTGCGTGAAGTGAAAAAGGAC	161	

Search completed: August 27, 2003, 23:58:10
Job time : 3117 secs

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Db	339	ACGGCGTGGCGGCTTGGCCCTTGGCCAGGAGGCGCTTCCACCGCTTCAGGCCACT	398
QY	822	ATCCGTACTGCAGACAGAGATGACCTGCCACCCACCATCTGGCTTCAGAGCGGGAGG	881
Db	399	ATCCGTACTGCAGACAGAGATGACCTGGCCACCCACCATCTGGCTTCAGAGCGGGAGG	458
QY	882	AGCCCCACCCCTCCAGAGGGGCCCTGGCACCCCTCCAGCTTCGGGAGCCCGACAGCAGCTGG	941
Db	459	AGCCCCACCCCTCCAGAGGGGCCCTGGCACCTCCAGCTTCGGGAGCCCGACAGCAGCTGG	518
QY	942	AACCTGAACCGGAGATCGGTCCGGCCGCCACCCCAACAGAACCATCTTCGACAGTACCTGA	1001
Db	519	AACCTGAACCGGAGATCGGTCCGGCCGCCACCCCAACAGAACCATCTTCGACAGTACCTGA	578
QY	1002	TGGATTACTGCCAGGCTGGGGCGGGCCCCCGCCACAGTAATCTCGGGGCTCAGGGCCA	1061
Db	579	TGGATTACTGCCAGGCTGGGGCGGGCCCCCGCCACAGTAATCTCGGGGCTCAGGGCCA	638
QY	1062	CGTACTCAGCGAGCGGGCGGGCGCATGTGAGAGGGGCCCGGCCCACTACAGCAGGATCATCG	1121
Db	639	CGTACTCAGCGAGCGGGCGGGCGCATGTGAGAGGGGCCCGGCCCACTACAGCAGGATCATCG	698
QY	1122	GCCACTACCGGGGGTCTCTCTTCCAGCACACAGCAGAGCATGTGGGGCCGGCTCTCTTGGTGG	1181
Db	699	GCCACTACCGGGGGTCTCTCTTCCAGCACACAGCAGAGCATGTGGGGCCGGCTCTCTTGGTGG	758
QY	1182	AGGGGAGCCCGGCTCCACCACACACATCATGCGGCCCTTAGAGAGGGCAGCATTCTGAGACA	1241
Db	759	AGGGGAGCCCGGCTCCACCACACACATCATGCGGGCCCTTAGAGAGGGCAGCATTCTGAGACA	818
QY	1242	AAGAGAAAGATTAACACAGAAAGACACCTCTCTTAGGTGCCACAGGGGGGCCGGGCTGGGG	1301
Db	819	AAGAGAAAGATTAACACAGAAAGACACCTCTCTTAGGTGCCACAGGGGGGCCGGGCTGGGG	878
QY	1302	CTGGCTAGTGGAAAAAGGCAG 1321	
Db	879	CTGGCTAGTGGAAAAAGGCAG 898	

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1      RESULT 2
2      US-09-769-482-2
3      Sequence 2, Application US/09769482
4      Patent No. 6566130
5      GENERAL INFORMATION:
6      APPLICANT: SRIVASTAVA, SHIV
7      APPLICANT: MOUL, JUDD W.
8      APPLICANT: XU, LINDA L.
9      APPLICANT: SEGAWA, TAKEHIKO
10     TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
11     FILE REFERENCE: 04995.0057-00000
12     CURRENT APPLICATION NUMBER: US/09/769,482
13     CURRENT FILING DATE: 2001-01-26
14     PRIOR APPLICATION NUMBER: 60/178,772
15     PRIOR FILING DATE: 2000-01-28
16     PRIOR APPLICATION NUMBER: 60/179,045
17     PRIOR FILING DATE: 2000-01-31
18     NUMBER OF SEQ ID NOS: 67
19     SOFTWARE: PatentIn Ver. 2.1
20     SEQ ID NO 2
21     LENGTH: 759
22     TYPE: DNA
23     ORGANISM: Homo sapiens
24     US-09-769-482-2

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Query Match	57.2%	Score 755	DB 4	Length 759
Best Local Similarity	100.0%	Pred. No. 1.7e-313		
Matches 755	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	522	CGAGCTGAGTTTGTTCAGATCATCATCTGCTGATATGATNGGANGGANGGCGG	581
Db	5	CGAGCTGAGTTTGTTCAGATCATCATCTGCTGATATGATNGGANGGANGGCGG	64

OY	582	TGATCAGTGCGCTCTTAGCCATCAACAAGCTGTGCAACGGTCCCTTATCAGCGGGACA	641
Db	65	TGATCAGTGCGCTCTTAGCCATCAACAAGCTGTGCAACGGTCCCTTATCAGCGGGACA	124
OY	642	GCCAGGGGCGAGGAGAGAAAGATGCCCTGTCTCAGAAAGATGCCCTGTGGCCTCGGAGA	701
Db	125	GCCAGGGGCGAGGAGAGAAAGATGCCCTGTCTCAGAAAGATGCCCTGTGGCCTCGGAGA	184
OY	702	GCAAGTGTCAAGGAAAGGAAATCCAGAGCGGCAAGTGTACGGCCCGCTCGGGCCACCG	761
Db	185	GCAAGTGTCAAGGAAAGGAAATCCAGAGCGGCAAGTGTACGGCCCGCTCGGGCCACCG	244
OY	762	ACCCGCTGGCCGTGCGCCCTTTCGCCACAGCGGAGCGCTTCACCGCTTCCAGCCCACT	821
Db	245	ACCCGCTGGCGGTGCGCCCTTTCGCCACAGCGGAGCGCTTCACCGCTTCCAGCCCACT	304
OY	822	ATCCGTACTCTCAGACAGAGATTCGACCTTCGCCACCCACCATCTGCTGTGCACAGGGGAGG	881
Db	305	ATCCGTACTCTCAGACAGAGATTCGACCTTCGCCACCCACCATCTGCTGTGCACAGGGGAGG	364
OY	882	AGCCCCACCCCTACAGAGGGGCCCTTCACACCTTCAGGACCTTCGGAGCCCGAGCAGCTGG	941
Db	365	AGCCCCACCCCTACAGAGGGGCCCTTCACACCTTCAGGACCTTCGGAGCCCGAGCAGCTGG	424
OY	942	AACTGAACCGGGAGTTCGGTGCAGCGCACCCCAAGAAACATCTTTCAGAGTGAACCTCGA	1001
Db	425	AACTGAACCGGGAGTTCGGTGCAGCGCACCCCAAGAAACATCTTTCAGAGTGAACCTCGA	484
OY	1002	TGGATAGTGCAGAGTGTGGGGCGGCCCTCCGCCCCAGCAGATGAATCTGGGGCATCAGCGCA	1061
Db	485	TGGATAGTGCAGAGTGTGGGGCGGCCCTCCGCCCCAGCAGATGAATCTGGGGCATCAGCGCA	544
OY	1062	CGTGTACTACGCGACGCGCGGGGCCCATATGAGAGGGGCGCGCCGCCCACTACAGCGAGTCAATCG	1122
Db	545	CGTGTACTACGCGCGCGGGGCCCATATGAGAGGGGCGCGCGCCGCCCACTACAGCGAGTCAATCG	604
OY	1122	GCCACTACCCGGGGGTCTCTCTTCAGAGCACACAGCAGAGTGGGGCGGCCCTCTCTCTGTGG	1181
Db	605	GCCACTACCCGGGGGTCTCTCTTCAGAGCACACAGCAGAGTGGGGCGGCCCTCTCTCTGTGG	664
OY	1182	AGGGGACCGCGCTCCACACACACACATCGCGCCCTTAGAGAGCGCAGCATCTGGAGCA	1241
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OY	1242	AAGAGAAGATTAACAGAAAGAGCAACCCCTCTAG	1276
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Sequence 1, Application US/0751891B
Patent No. 6180337
GENERAL INFORMATION:
APPLICANT: Caskey, C. T.
Nelson, David L.
Pieretti, Maura
Warren, Stephen T.
Costra, Ben A.
Fu, Ying-hui
TITLE OF INVENTION: Diagnosis of the Fragile X Syndrome
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas D. Paul
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/751,891B
FILING DATE: 29-Aug-1991
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32, 714
REFERENCE/DOCKET NUMBER: D-5350
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
TELEX: 762829
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3765 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-07-751-891B-1
Query Match 2.1%; Score 28; DB 3; Length 3765;
1st Local Similarity 100.0%; Pred 0.0052;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY 56 GCGCGCGCGCGCGCGCGCGCGCGAGGCG 83
|||||
DB 44 GCGCGCGCGCGCGCGCGCGCGCGAGGCG 71

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ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,073A
FILING DATE: 31-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: JPN-2201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4362 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 220..2118
US-08-455-073A-1

Query Match 2.1% Score 28; DB 2; Length 4362;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 56 GCGCGCGCGCGCGCGCGCGCGCGGAGCG 83
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Db 68 GCGCGCGCGCGCGCGCGCGCGCGGAGCG 95

RESULT 8
US-08-457-273B-41/c
Sequence 41, Application US/08457273B
Patent No. 5849995
GENERAL INFORMATION:
APPLICANT: Hayden, Michael
APPLICANT: Iln, Biaoyang
APPLICANT: Nasir, Jamal
TITLE OR INVENTION: Mouse Model for Huntington's Disease and
TITLE OF INVENTION: Related DNA Sequences
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Virginia Bennett
STREET: PO Box 37428
CITY: Raleigh
STATE: No. 5849995th Carolina
COUNTRY: US
ZIP: 27627
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,273B
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,092
REFERENCE/DOCKET NUMBER: 3477-85A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-854-1400
TELEFAX: 919-854-1401
INFORMATION FOR SEQ ID NO: 41:

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LOCATION: 316..9748
US-08-246-982A-5

Query Match 2.1%; Score 28; DB 1; Length 10366;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 51 GAGGAGCGCGCGCGCGCGCGCG 78
DB 469 GAGGAGCGCGCGCGCGCGCGCG 442

RESULT 12
US-08-453-265-5/c
Sequence 5, Application US/08453265
Patent No. 5693757
GENERAL INFORMATION:
APPLICANT: MacDonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntington DNA, Protein And Uses Thereof
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,265
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609,3880003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10366 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

FEATURE:
NAME/KEY: CDS
LOCATION: 316..9748
US-08-453-265-5

Query Match 2.1%; Score 28; DB 1; Length 10366;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 51 GAGGAGCGCGCGCGCGCGCGCG 78
DB 469 GAGGAGCGCGCGCGCGCGCGCG 442

RESULT 13
US-09-325-932A-2/c
Sequence 2, Application US/09325932A
Patent No. 6451604
GENERAL INFORMATION:
APPLICANT: Flynn, Barry
APPLICANT: Lasham, Annette

TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant dev
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 367
TYPE: DNA
ORGANISM: Pinus radiata
US-09-325-932A-2

Query Match 2.0%; Score 26; DB 4; Length 367;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 56 GCGCGCGCGCGCGCGCGCGCGCG 81
DB 367 GCGCGCGCGCGCGCGCGCGCGCG 342

RESULT 14
US-09-780-173A-10
Sequence 10, Application US/09780173A
Patent No. 6455307
GENERAL INFORMATION:
APPLICANT: Robert McKay
APPLICANT: Susan M. Freier
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-ALPHA PRIME EXPRESSION
FILE REFERENCE: RTS-0165
CURRENT APPLICATION NUMBER: US/09/780,173A
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 95
SEQ ID NO 10
LENGTH: 1877
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (344)...(1396)
US-09-780-173A-10

Query Match 2.0%; Score 26; DB 4; Length 1877;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 380 CCGCGCGCGCGCGCGCGCGCGCG 405
DB 278 CCGCGCGCGCGCGCGCGCGCGCG 303

RESULT 15
US-08-819-177-2/c
Sequence 2, Application US/08819177
Patent No. 6043083
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Dickens, Martin
TITLE OF INVENTION: INHIBITORS OF THE JNK SIGNAL
TITLE OF INVENTION: TRANSDUCTION PATHWAY AND METHODS OF USE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible


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OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,177
FILING DATE: 28 April 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/037001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2832 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 180...2159
OTHER INFORMATION: JIP-1 cDNA
US-08-819-177-2

Query Match      2.0%; Score 26; DB 3; Length 2832;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      53 GGAGGCGGCGGCGGCGGCGGCGGCGG 78
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Db      138 GGAGGCGGCGGCGGCGGCGGCGGCGG 113
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Job time : 100 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 27, 2003, 23:06:11 ; Search time 367 Seconds
(without alignments)
8258.053 Million cell updates/sec

Title: US-09-934-249-1

Perfect score: 1321
Sequence: 1 cgaccgcgctcgcgagcga.....ctgcgtagtgtaaaagcag 1321

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1533700 seqs, 1147125425 residues

Hit size : 8

Total number of hits satisfying chosen parameters: 2240168

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1321	100.0	1321	US-09-934-249-1	Sequence 1, Appl1
2	1329	93.0	4839	US-10-241-220-119	Sequence 119, App
3	861	65.2	861	US-09-934-249-3	Sequence 3, Appl1
4	800	60.6	1141	US-10-301-822-208	Sequence 208, App
5	800	60.6	1141	US-10-205-823-412	Sequence 412, App
6	800	60.6	1850	US-10-241-220-44	Sequence 44, Appl
7	788	59.7	1066	US-10-098-841-71	Sequence 71, Appl
8	749	56.7	969	US-09-796-753-55	Sequence 55, Appl
9	713	54.0	806	US-10-241-220-45	Sequence 45, Appl
10	560	42.4	1583	US-10-000-256A-32	Sequence 32, Appl
11	302	22.9	693	US-09-934-249-14	Sequence 14, Appl
12	178	13.5	467	US-09-918-995-2074	Sequence 2074, Ap
13	102	7.7	368	US-09-783-590-3464	Sequence 3464, Ap
14	50	3.8	65	US-09-783-590-3488	Sequence 3488, Ap
15	44	3.3	878	US-09-934-249-12	Sequence 12, Appl
16	44	3.3	1713	US-09-796-753-57	Sequence 57, Appl

17	41	3.1	475	10	US-09-934-249-15	Sequence 15, Appl
18	32	2.4	577	9	US-09-864-761-20542	Sequence 20542, A
19	32	2.4	1206	12	US-10-259-165-327	Sequence 327, App
20	32	2.4	1964	9	US-09-864-761-3776	Sequence 3776, Ap
21	29	2.2	401	9	US-09-864-761-3936	Sequence 3936, Ap
22	29	2.2	446	9	US-09-864-761-20699	Sequence 20699, A
23	29	2.2	1128	11	US-09-836-960-1	Sequence 1, Appl1
24	29	2.2	1277	13	US-10-062-254-279	Sequence 279, Appl
25	29	2.2	1570	11	US-09-836-960-4	Sequence 4, Appl1
26	29	2.2	2853	14	US-09-905-983-45	Sequence 45, Appl1
27	29	2.2	2853	14	US-10-177-293-42	Sequence 42, Appl
28	29	2.2	2887	12	US-10-017-621-89	Sequence 89, Appl
29	28	2.1	204	14	US-10-215-432-29	Sequence 29, Appl
30	28	2.1	251	14	US-10-060-036-418	Sequence 418, App
31	28	2.1	412	10	US-09-960-352-13161	Sequence 13161, A
32	28	2.1	496	10	US-09-783-590-3813	Sequence 3813, Ap
33	28	2.1	614	14	US-10-215-432-30	Sequence 30, Appl
34	28	2.1	614	14	US-10-215-432-31	Sequence 31, Appl
35	28	2.1	840	14	US-10-259-165-762	Sequence 762, App
36	28	2.1	1080	14	US-10-215-432-26	Sequence 26, Appl
37	28	2.1	15698	12	US-09-879-312-1	Sequence 1, Appl1
38	28	2.1	1303	10	US-10-311-455-2114	Sequence 2114, Ap
39	27	2.0	402	10	US-09-738-973-418	Sequence 418, App
40	27	2.0	402	10	US-09-854-133-418	Sequence 418, App
41	27	2.0	402	14	US-10-144-649A-418	Sequence 418, App
42	27	2.0	428	10	US-09-920-455-62	Sequence 62, Appl
43	27	2.0	1041	27	US-10-177-293-285	Sequence 285, App
44	27	2.0	1161	10	US-09-833-381-2046	Sequence 2046, Ap
45	27	2.0	1403	13	US-10-098-841-280	Sequence 280, App

ALIGNMENTS

US-09-934-249-1
Sequence 1, Application US/09934249
Patent No. US20020115081A1
GENERAL INFORMATION:
APPLICANT: Lee, Richard T.
APPLICANT: Landschultz, Katherine T.
APPLICANT: Turil, Thomas G.
APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
FILE OF INVENTION: CARDIOVASCULAR CONDITIONS
FILE REFERENCE: P0738/001/ERP/KA
CURRENT APPLICATION NUMBER: US/09/934, 249
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227, 159
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FASTED for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1321
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (413)...(1273)
US-09-934-249-1

Query Match 100.0%; Score 1321; DB 10; Length 1321;
Best local similarity 100.0%; Pred. No. 0;
Matches 1321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGACGCGGCTCGAGCGAAACCCGATCTCTTGACTTGATGAGAGAGAGCGG 60
DB 1 CGACGCGGCTCGAGCGAAACCCGATCTCTTGACTTGATGAGAGAGAGCGG 60
QY 61 CGGCGGCGGCGGCGGCGGAGGCGCTGCGTGGGGAAGCTACGCGAGAGCTCAGCCCC 120
DB 61 CGGCGGCGGCGGCGGCGGAGGCGCTGCGTGGGGAAGCTACGCGAGAGCTCAGCCCC 120

OY	573	TGCGTGGTGATACAGTCCTGTGTGAAGCCACTCAAGCTGTCTGCACAGGTCCTTCAATCA	632
Dd	481	TTTTTTTTTTTGGTGATATACAGTCCTGTGTGAAGCCACTCAAGCTGTCTGCACAGGTCCTTCAATCA	540
OY	633	GCCCGCACAGCAGCAGGGCGAGAGAGAAGATGCCCTGTCTCTAGAAAGATCCTGTGGC	692
Dd	541	GGCGGCACAGCCAGGGGGGAGAGAGAAGATGGCTGTCTCTAGAAAGATCCTGTGGC	600
OY	693	CCTTGGAGAGACACAGTGTCAAGGCACAGGAATCCAGAGCCGACAGTCTACGCCGCCCTC	752
Dd	601	CCTTGGAGAGAGACAGTGTCAAGGCACAGGAATCCAGAGCCGACAGTCTACGCCGCCCTC	660
OY	753	GGCCCCACGAGCCGCTGGCCGTGCGGCCCTTGGCCCCAGCGGAGACGGTTCACCAGGCTTC	812
Dd	661	GGCCCCACGAGCCGCTGGCCGTGCGGCCCTTGGCCCCAGCGGAGACGGTTCACCAGGCTTC	720
OY	813	AGCCACACTTATCCCTACTCTGCAGCAGAGATGACACTGACACCACCATCTCGCTGTACAG	872
Dd	721	AGCCACACTTATCCCTACTCTGCAGCAGAGATGACACTGACACCACCATCTCGCTGTACAG	780
OY	873	ACGGGGAGAGAGCCCCCACAACCTTACAGAGGCCCTTGCACCTTCACAGCTTCGGGAGCCCCGAGC	932
Dd	781	ACGGGGAGAGAGCCCCCACAACCTTACAGAGGCCCTTGCACCTTCACAGCTTCGGGAGCCCCGAGC	840
OY	933	AGCAGCTGGAACTGAACCGGGAGTCCGGTGGCGGCGACGCCCAAAGAAACCATCTTCGACGA	992
Dd	841	AGCAGCTGGAACTGAACCGGGAGTCCGGTGGCGGCGACGCCCAAAGAAACCATCTTCGACGA	900
OY	993	GTGACCTGATGGATAGTAGTCCAGAGCTGGGGCGGCCCTTGCACCCGCCAGCAGTAACTCGGGCA	1052
Dd	901	GTGACCTGATGGATAGTAGTCCAGAGCTGGGGCGGCCCTTGCACCCGCCAGCAGTAACTCGGGCA	960
OY	1053	TCACGCCACAGTGTACGGCAGCGCGGGCGGCATGAGAGGGGCCCGGCCACTTAACAGCG	1112
Dd	961	TCACGCCACAGTGTACGGCAGCGCGGGCGGCATGAGAGGGGCCCGGCCACTTAACAGCG	1020
OY	1113	AGGTATATCGGCGCACTACCCGGGGTCTCTCTCCAGACACAGCAGAGCAGTGGGCGGCCCT	1172
Dd	1021	AGGTATATCGGCGCACTACCCGGGGTCTCTCTCCAGACACAGCAGAGCAGTGGGCGGCCCT	1080
OY	1173	CCTTGTGTGAGAGGAGCCCGGCTCCACACACACACATCGCGCCCTTAGAGAGCGCAGCCA	1232
Dd	1081	CCTTGTGTGAGAGGAGCCCGGCTCCACACACACACATCGCGCCCTTAGAGAGCGCAGCCA	1140
OY	1233	TCCTGAGCAAAAGAAAGATTAACAAGAAAGACACCTCTTAGGGTCTCCAGGGGGGCC	1292
Dd	1141	TCCTGAGCAAAAGAAAGATTAACAAGAAAGACACCTCTTAGGGTCTCCAGGGGGGCC	1200
OY	1293	GGGCTGGGGCTGCTAGGTGAAAAAGGCG	1321
Dd	1201	GGGCTGGGGCTGCTAGGTGAAAAAGGCG	1229
RESULT 3			
US-09-934-249-3			
Sequence 3, Application US/09934249			
Patent No. US20020115081A1			
GENERAL INFORMATION:			
APPLICANT: Lee, Richard T.			
APPLICANT: Landschultz, Katherine T.			
APPLICANT: Turf, Thomas G.			
APPLICANT: Thompson, John F.			
APPLICANT: Kennedy, Scott P.			
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF			
TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS			
FILE REFERENCE: P0738/77001/ERP/VA			
CURRENT FILING DATE: US/09/934.249			
PRIOR APPLICATION NUMBER: 2001-08-21			
PRIOR FILING DATE: 2000-08-22			
NUMBER OF SEQ ID NOS: 17			
SOFTWARE: FastSeq for Windows Version 3.0			

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US-RESULT 4
US-10-301-822-208
; Sequence 208, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MPM01-029P2RM
; CURRENT APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (96) ... (854)
US-10-301-822-208

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY    522 CGGAGCTTGAGTTTGTTCAGATCATCATCATCGTGGTGTGATGATGATGATGATGATG 581
DB    100 CGGAGCTGAGATTGTGTTCAGATCATCATCATCGTGGTGTGATGATGATGATGATGATG 159

QY    582 TGATCAGCTGCCTGCTGTGAAGCCACTCAAAAGCTGTGTACAGCGSTCTTATCACGCGGACA 641
DB    160 TGAATCAGCTGCCTGCTGTGAAGCCACTCAAAAGCTGTGTACAGCGSTCTTATCACGCGGACA 219

QY    642 GCACAGGCGGAGAGAGAATAATGACCCTGCTCTGAGAAGATGCTGTGAGCCCTTGAGAGA 701
DB    220 GCCAGGCGGAGAGAGAATAATGAGTGCTGTCTCTGAGAAGATGCTGTGTGAGCCCTTGAGAGA 279

QY    702 GCACAGTGTACGAGCAACGAAATCCCAGAGCCGACAGTGTACGCCGCCGCTTGCCCCACCG 761
DB    280 GCACAGTGTACGAGCAACGAAATCCCAGAGCCGACAGTGTACGCCGCCGCTTGCCCCACCG 339

QY    762 ACCGCTGTGGCGCTGCCGCCCTTGCCCGCCAGCGGAGACGGCTTCCACCGCTTCCAGCCACCT 821
DB    340 ACCGCTGTGGCGCTGCCGCCCTTGCCCGCCAGCGGAGACGGCTTCCACCGCTTCCAGCCACCT 399

QY    822 ATCCGTACTCTCAGACGACGATTCGACTCTCCACCCACCACCATCTCGCTGTACAGCGGGAGAG 881
DB    400 ATCCGTACTCTCAGACGACGATTCGACTCTCCACCCACCACCATCTCGCTGTACAGCGGGAGAG 459

QY    882 AGCCCCAACCTTACCAAGGCCCCCTTCACACCTTCACAGCTTCGGGAAACCCCGAGACGACGTGG 941
DB    460 AGCCCCAACCTTACCAAGGCCCCCTTCACACCTTCACAGCTTCGGGAAACCCCGAGACGACGTGG 519

QY    942 AACTGTAACCGGAGATCGGTGGCGGACACCCCAAAGAAACATCTTCGACAGTAGCAGTGA 1001
DB    520 AACTGTAACCGGAGATCGGTGGCGGACACCCCAAAGAAACATCTTCGACAGTAGCAGTGA 579
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OY	1002	TGGATGATGCCAGGCTGGGGCGCCCGCCCCCCCACAGTAAGTATCGGGATCAGCCCA	1068
Dd	580	TGGATGATGCCAGGCTGGGGCGCCCGCCCCCCCACAGTAAGTATCGGGATCAGCCCA	639
OY	1062	CGTCTACTAGCAGCGGGGGGCATGTGAGGGGGCGCCGCCACTACAGGAGGTCAATCG	1121
Dd	640	CGTCTAAGGAGCGGGGGGCATGTGAGGGGGCGCCGCCACTACAGGAGGTCAATCG	699
OY	1122	GCCACTACCGGGGGTCTCTCTTCACAGCACAGACAGCATGTGGGGCGCCCTTGCTGG	1181
Dd	700	GCCACTACCGGGGGTCTCTCTTCACAGCACAGACAGCATGTGGGGCGCCCTTGCTGG	759
OY	1182	AGGGGACCCGGCTCCACCACACACATCGCGCCCTAGAGAGCGCAGCATCTGGAGA	1241
Dd	760	AGGGGACCCGGCTCCACCACACACATCGCGCCCTAGAGAGCGCAGCATCTGGAGA	819
OY	1242	AAGAGAAAGATTAACAAGAAAGAACCCCTCTTAGGTGCCAGGGGGCGGGCTGGGG	1301
Dd	820	AAGAGAAAGATTAACAAGAAAGAACCCCTCTTAGGTGCCAGGGGGCGGGCTGGGG	879
OY	1302	CTGCGTAGTGATAAAGCGAG	1321
Dd	880	CTGCGTAGTGATAAAGCGAG	899
 RESULT 5 US-10-205-823-412			
; Sequence 412, Application US/10205823			
; Publication No. US20030108963A1			
; GENERAL INFORMATION:			
; APPLICANT: Schlegel, Robert			
; APPLICANT: Monahan, John E.			
; APPLICANT: Endege, Wilson O.			
; APPLICANT: Ganavarapu, Manjula			
; APPLICANT: Goebachaya, Bella			
; APPLICANT: Hoersch, Sebastian			
; APPLICANT: Kamalakar, Shudhangl			
; APPLICANT: Monsey, Angela M.			
; APPLICANT: Glatt, Karen			
; APPLICANT: Zhao, Xumel			
; APPLICANT: Anderson, Dustin			
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND			
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND			
; FILE OF INVENTION: THERAPY OF PROSTATE CANCER			
; FILE REFERENCE: MRI-044			
; CURRENT APPLICATION NUMBER: US/10/205, 823			
; CURRENT FILING DATE: 2002-07-25			
; PRIOR APPLICATION NUMBER: 60/307, 982			
; PRIOR FILING DATE: 2001-07-25			
; PRIOR APPLICATION NUMBER: 60/314, 356			
; PRIOR FILING DATE: 2001-08-22			
; PRIOR APPLICATION NUMBER: 60/325, 020			
; PRIOR FILING DATE: 2001-09-25			
; PRIOR APPLICATION NUMBER: 60/341, 746			
; PRIOR FILING DATE: 2001-12-12			
; PRIOR APPLICATION NUMBER: 60/362, 158			
; PRIOR FILING DATE: 2002-03-05			
; NUMBER OF SEQ ID NOS: 455			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 412			
; LENGTH: 1141			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; US-10-205-823-412			
 Query Match 60.6%: Score 800; DB 14; Length 1141;			
Best Local Similarity 100.0%: Pred. No. 0; Indels 0; Gaps 0;			
Matches 800; Conservative 0; Mismatches 0; 0; 0;			
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Dd	100	CGGACTGAGATTGTCAGATCATCATCATCATGTTGGTGAATGATGATGATGATGATG	159

APPLICANT: Asundi, Vinod
 APPLICANT: Xu, Chongjun
 APPLICANT: Zhou, Ping
 APPLICANT: Ma, Yungqing
 APPLICANT: Wang, Jian-Rui
 APPLICANT: Zhao, Qing A.
 APPLICANT: Ren, Feiyan
 APPLICANT: Chen, Rui-hong
 APPLICANT: Wang, Duntui
 APPLICANT: Wang, Zhiwei
 APPLICANT: Wehrman, Tom
 APPLICANT: Zhang, Jie
 APPLICANT: Qian, Xiaohong B.
 APPLICANT: Drmanac, Radoje T.
 TITLE OF INVENTION: No. US20020197679a1el Nucleic Acids and
 FILE REFERENCE: 784CIP2
 CURRENT APPLICATION NUMBER: US/10/098,841
 CURRENT FILING DATE: 2002-03-13
 PRIOR APPLICATION NUMBER: 09/598,042
 PRIOR FILING DATE: 2000-06-20
 PRIOR APPLICATION NUMBER: 09/552,317
 PRIOR FILING DATE: 2000-04-25
 PRIOR APPLICATION NUMBER: 09/488,725
 PRIOR FILING DATE: 2000-01-21
 NUMBER OF SEQ ID NOS: 331
 SOFTWARE: PL_genes Version 1.0
 SEQ ID NO 71
 LENGTH: 1066
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (134)..(867)
 US-10-098-841-71

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Dd		605	GGCTGGGAGGGCCCTTGCCCCCAGCAAGTACTCGGGGATCATGGGCCACGGTGCATTACGGACA	664
Oy		1074	GCGGCGGGGCGCATGGAGGGGGCCCGCCACCTTACAGCGAGGTATGGCCACTTAACC	1133
Dd		665	GCGGCGGGGCGCATGGAGGGGGCCCGCCACCTTACAGCGAGGTATGGCCACTTAACC	724
Oy		1134	GGTCCTCTCTTCCACACAGCAGAGCAGTAGTGGGCGCCCTCTTCTGTGGAGGGGACCCGGC	1193
Dd		725	GGTCCTCTCTTCCACACAGCAGAGCAGTAGTGGGCGCCCTCTTCTGTGGAGGGGACCCGGC	784
Oy		1194	TCCACCAACACACATGCGCGCCCTTAAGAGCGACGCCATCTGGAGCAAAAGAGAAGATA	1253
Dd		785	TCCACCAACACACATGCGCGCCCTTAAGAGCGACGCCATCTGGAGCAAAAGAGAAGATA	844
Oy		1254	AACGAAGAAGCACACCTCTCTTAAGGGTCCCACAGGGGGGGCGGGGCTGCGTAAGGGA	1313
Dd		845	AACGAAGAAGCACACCTCTCTTAAGGGTCCCACAGGGGGGGCGGGGCTGCGTAAGGGA	904
Oy		1314	AAAAAGCAG 1321	
Dd		905	AAAAGCAG 912	
 RESULT 8 US-09-796-753--55 ; Sequence 55, Application US/09796753 ; Publication No. US20030027998A1 GENERAL INFORMATION: APPLICANT: McCarthy, Sean A. TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF FILE REFERENCE: 7853-227-999 CURRENT APPLICATION NUMBER: US/09/796,753 CURRENT FILING DATE: 2001-03-01 PRIOR APPLICATION NUMBER: 09/183,175 PRIOR FILING DATE: 1998-10-30 PRIOR APPLICATION NUMBER: 09/223,094 PRIOR FILING DATE: 1998-12-30 PRIOR APPLICATION NUMBER: 09/223,546 PRIOR FILING DATE: 1998-12-30 PRIOR APPLICATION NUMBER: 09/224,246 PRIOR FILING DATE: 1998-12-30 PRIOR APPLICATION NUMBER: 09/259,388 PRIOR FILING DATE: 1999-02-26 PRIOR APPLICATION NUMBER: 60/122,458 PRIOR FILING DATE: 1999-03-01 PRIOR APPLICATION NUMBER: 09/312,359 PRIOR FILING DATE: 1999-05-14 PRIOR APPLICATION NUMBER: 09/336,536 PRIOR FILING DATE: 1999-06-18 PRIOR APPLICATION NUMBER: 09/342,687 PRIOR FILING DATE: 1999-06-29 PRIOR APPLICATION NUMBER: 09/345,464 PRIOR FILING DATE: 1999-06-30 PRIOR APPLICATION NUMBER: 09/365,164 PRIOR FILING DATE: 1999-07-30 PRIOR APPLICATION NUMBER: 09/399,723 PRIOR FILING DATE: 1999-09-20 PRIOR APPLICATION NUMBER: 09/409,634 PRIOR FILING DATE: 1999-09-30 PRIOR APPLICATION NUMBER: 09/471,179 PRIOR FILING DATE: 1999-12-23 PRIOR APPLICATION NUMBER: 09/474,071 PRIOR FILING DATE: 1999-12-29 PRIOR APPLICATION NUMBER: 09/474,072 PRIOR FILING DATE: 1999-12-29 PRIOR APPLICATION NUMBER: 09/514,010 PRIOR FILING DATE: 2000-02-25 PRIOR APPLICATION NUMBER: 09/516,745 PRIOR FILING DATE: 2000-03-01 PRIOR APPLICATION NUMBER: 09/572,002 PRIOR FILING DATE: 2000-05-14 PRIOR APPLICATION NUMBER: 09/597,993				

Thu Aug 28 08:39:18 2003

us-09-934-249-1.018.rmp

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DB 1187 GGGGCGCCGCCACCTACAGAGGTATCGGCCACCTACCCGGGGTCTCTTCAGCA 1246
QY 1150 CCAGCAGAGAGTGGGGCCCTCTCTTGGAGGGGACCCGGCTCCAGCAGACAT 1209
DB 1247 CCAGCAGAGAGTGGGGCCCTCTCTTGGAGGGGACCCGGCTCCAGCAGACAT 1306
QY 1210 GCGGCGCTTACAGAGCCGACCATCTGAGCAAGAGAGATTAACAGAAAGACACC 1269
DB 1307 GCGGCGCTTACAGAGCCGACCATCTGAGCAAGAGAGATTAACAGAAAGACACC 1366
QY 1270 TCTTAGGGTCCCGAGGGG 1289
DB 1367 TCTTAGGGTCCCGAGGGG 1386

RESULT 11
US-09-934-249-14/c
Sequence 14, Application US/09934249
Patent No. US20020115081A1
GENERAL INFORMATION:
APPLICANT: Lee, Richard T.
APPLICANT: Landshultz, Katherine T.
APPLICANT: Turt, Thomas G.
APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
FILE REFERENCE: P0738/7001/ERP/KA
CURRENT APPLICATION NUMBER: US/09/934,249
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR FILING DATE: 2000-08-22
SOFTWARE: FastSeq for Windows Version 3.0
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 14
LENGTH: 693
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: (639)
OTHER INFORMATION: a, c, g, or t/u
US-09-934-249-14

Query Match 22.9%; Score 302; DB 10; Length 693;
Best Local Similarity 100.0%; Pred. No. 8.6e-137; Indels 0; Gaps 0;
Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 885 CCCGACCTACAGAGGCGCCCTGACCTGACCTTGGGAGCCCGAGAGCAGAGCTGGAGC 944
DB 587 CCCGACCTACAGAGGCGCCCTGACCTGACCTTGGGAGCCCGAGAGCAGAGCTGGAGC 528
QY 945 TGAACGGGAGTGGTGGCGGACCCCAACAGAACATCTTGACAGTGAATGG 1004
DB 527 TGAACGGGAGTGGTGGCGGACCCCAACAGAACATCTTGACAGTGAATGG 468
QY 1005 ATAGTGCAGAGTGGGCGCCCTGACCTGACCTTGGGAGCCCGAGAGCAGAGCTGGAGC 1064
DB 467 ATAGTGCAGAGTGGGCGCCCTGACCTGACCTTGGGAGCCCGAGAGCAGAGCTGGAGC 408
QY 1065 GCTACGAGAGGGGGGCGATGAGAGGGGCGCCGACCTACAGAGAGTGAATGG 1124
DB 407 GCTACGAGAGGGGGGCGATGAGAGGGGCGCCGACCTACAGAGAGTGAATGG 348
QY 1125 ACTACCGGGGTCTCTTCCAGCAGCAGAGAGAGTGGGCGCCCTGCTGTGAGG 1184
DB 347 ACTACCGGGGTCTCTTCCAGCAGCAGAGAGAGTGGGCGCCCTGCTGTGAGG 288
QY 1185 GG 1186
DB 287 GG 286
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DB 517 TGGATAGTCCAGAGGCTGGGGCCCTTCCGCCAGCAGTAATCGGGCATCAGGCCCA 576
QY 1062 CTGTCTACAGGCGAGCGGGCGCATGAGAGGGCGCCGCCAGCTACAGAGAGTCAATCG 1121
DB 577 CTGTCTACAGGCGAGCGGGCGCATGAGAGGGCGCCGCCAGCTACAGAGAGTCAATCG 636
QY 1122 GCCACTACCGGGGCTCTCTTCCAGCAGCAGAGAGTGGGGCGCCCTCTGTCTGG 1181
DB 637 GCCACTACCGGGGCTCTCTTCCAGCAGCAGAGAGTGGGGCGCCCTCTGTCTGG 696
QY 1182 AGGGGACCGGGCTCCAGCAGCAGACATCGCGCCCTAGAGGCGCAGCATCTGAGCA 1241
DB 697 AGGGGACCGGGCTCCAGCAGCAGACATCGCGCCCTAGAGGCGCAGCATCTGAGCA 756
QY 1242 AAGAGAGATTAACAGAAAGAGACCCCTCTAGAGGTCCCGAG 1285
DB 757 AAGAGAGATTAACAGAAAGAGACCCCTCTAGAGGTCCCGAG 800

LT 10
US-10-000-256A-32
Sequence 32, Application US/10000256A
Publication No. US20030039983A1
GENERAL INFORMATION:
APPLICANT: Sun, Yongming
APPLICANT: Recipon, Herve
APPLICANT: Liu, Chenghua
APPLICANT: Chen, Sei-Yu
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
FILE REFERENCE: DEX-0259
CURRENT APPLICATION NUMBER: US/10/000,256A
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 60/244,782
PRIOR FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patent version 3.1
SEQ ID NO 32
LENGTH: 1583
TYPE: DNA
ORGANISM: Homo sapien
US-10-000-256A-32

Query Match 42.4%; Score 560; DB 14; Length 1583;
Best Local Similarity 100.0%; Pred. No. 2.9e-262; Indels 0; Gaps 0;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 730 GCCGAGGTACAGCGCCGCTCGCCACCGACCGCTTGGCGCGCCCTTGGCCCA 789
DB 827 GCCGAGGTACAGCGCCGCTCGCCACCGACCGCTTGGCGCGCCCTTGGCCCA 886
QY 790 GCGGAGCGCTTCCAGCGCTTCCAGCAGCAGTATCGTACGACAGATGACCT 849
DB 887 GCGGAGCGCTTCCAGCGCTTCCAGCAGCAGTATCGTACGACAGATGACCT 946
QY 850 GCCACCCACCATCTCGCTGTGACAGCGGAGAGAGCGCCCACTACAGAGGCGCCCTGAC 909
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QY 910 CTTTCAGCTTGGGAGCCCGAGAGAGTGAATGAACCGGAGTGGTGGCGGAC 969
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DB 1067 CCCAAGAGAGATCTTGGAGAGTGAATGATGAGTGGAGTGGGGCGCCCTG 1126
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RESULT 12
US-09-918-995-2074
; Sequence 2074, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2074
; LENGTH: 467
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(467)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-2074

Query Match 13.5%; Score 178; DB 11; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.7e-76;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1144 CCAGCACCAGAGAGCAGTGGGCGCCCTCTTGTGTGAGAGGAGCCGCGCTCCACACAC 1203
DB 36 CCACACACAGAGAGAGTGGGCGCCCTCTTGTGTGAGAGGAGCCGCGCTCCACACAC 95

QY 1204 ACACATGCGCGCCCTAGAGAGCGAGCCATCTGGAGCAAGAGATTAACAGAAAG 1263
DB 96 ACACATGCGCGCCCTAGAGAGCGAGCCATCTGGAGCAAGAGATTAACAGAAAG 155

QY 1264 ACACCTCTCTAGAGTCCCGAGGGGGCGGCTGGGGCTCGTAGGTGAAGGAGCAG 1321
DB 156 ACACCTCTCTAGAGTCCCGAGGGGGCGGCTGGGGCTCGTAGGTGAAGGAGCAG 213

RESULT 13
US-09-783-590-3464
; Sequence 3464, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16,2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3464
; LENGTH: 368
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (103)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (225)
; OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: misc_feature
LOCATION: (279)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (314)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (349)
OTHER INFORMATION: n equals a,t,g, or c
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LOCATION: (350)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (366)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (367)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (368)
OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-3464

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Best Local Similarity 100.0%; Pred. No. 1.6e-39;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 TACCGGGGCTCTCTTCCAGACAGAGAGTGGGCGCCCTCTTGTGTGAGAGG 60

QY 1187 ACCGGGCTCCACACACACATGCGCGCCCTAGAGAGCGGA 1228
DB 61 ACCGGGCTCCACACACACATGCGCGCCCTAGAGAGCGGA 102

RESULT 14
US-09-783-590-3488
; Sequence 3488, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16,2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3488
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (51)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-3488

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Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1127 TACCGGGGCTCTCTTCCAGACAGAGAGTGGGCGCCCTCTT 1176
DB 1 TACCGGGGCTCTCTTCCAGACAGAGAGTGGGCGCCCTCTT 50

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 27, 2003, 17:38:05; Search time 5026 Seconds

(without alignments)
10752.411 Million cell updates/sec

Title: US-09-934-249-1

Perfect score: 1321

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Gapop 10.0, Gapext 1.0

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database :

GenBank: 1: gb_da: 2: gb_hcg: 3: gb_in: 4: gb_om: 5: gb_ov: 6: gb_pat: 7: gb_ph: 8: gb_pl: 9: gb_pr: 10: gb_ro: 11: gb_sts: 12: gb_sy: 13: gb_un: 14: gb_vl: 15: em_da: 16: em_fun: 17: em_hum: 18: em_in: 19: em_mu: 20: em_om: 21: em_or: 22: em_ov: 23: em_pat: 24: em_ph: 25: em_pl: 26: em_ro: 27: em_sts: 28: em_un: 29: em_vl: 30: em_hcg_hum: 31: em_hcg_inv: 32: em_hcg_other: 33: em_hcg_mus: 34: em_hcg_pln: 35: em_hcg_rod: 36: em_hcg_mam: 37: em_hcg_vtl: 38: em_sy: 39: em_hcg_hum: 40: em_hcg_mus: 41: em_hcg_other:

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1321	100.0	1321	6	AX392417	AX392417 Sequence
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3	887.4	67.2	1061	9	BC015918	BC015918 Homo sapi
4	861	65.2	861	6	AX392419	AX392419 Sequence
5	802.2	60.7	1141	9	AF224278	AF224278 Homo sapi
6	800	60.6	1818	9	AY128643	AY128643 Homo sapi
7	630	47.7	1379	10	BC036995	BC036995 Mus muscu
8	616.4	45.7	878	6	AX392428	AX392428 Sequence
9	594.4	45.0	61505	9	AF305426	AF305426 Homo sapi
10	584.4	45.0	130435	9	HS71877	HS71877 Human DNA
11	589.2	44.6	1583	6	AX393655	AX393655 Sequence
12	522.8	39.6	150224	9	HSJ1059L7	AL121913 Human DNA
13	493.6	37.4	693	6	AX392430	AX392430 Sequence
14	425	32.2	651	10	AF220208	AF220208 Mus muscu
15	417.8	31.6	812	6	AX011709	AX011709 Sequence
16	401.4	30.4	408	6	AX071267	AX071267 Sequence
17	400.6	30.3	673	6	AX525744	AX525744 Sequence
18	377.2	28.6	156698	10	AL837509	AL837509 Mouse DNA
19	377.2	28.6	175754	2	AC110189	AC110189 Mus muscu
20	377.2	28.6	176821	2	AL837520	AL837520 Mus muscu
21	357.6	27.1	249554	2	AC139417	AC139417 Rattus no
22	357.6	27.1	258632	2	AC111878	AC111878 Rattus no
23	352.2	26.7	921	6	AR233384	AR233384 Sequence
24	352.2	26.7	8065	6	AR233383	AR233383 Sequence
25	352.2	26.7	8494	9	AF009424	AF009424 Homo sapi
26	350	26.5	2170	6	AX713513	AX713513 Sequence
27	350	26.5	2170	9	AK055028	AK055028 Homo sapi
28	349	26.4	8093	6	AX392432	AX392432 Sequence
29	349	26.4	8093	6	AF009426	AF009426 Homo sapi
30	341.8	25.9	475	6	AX392431	AX392431 Sequence
31	284.2	21.5	867	6	AR233385	AR233385 Sequence
32	284.2	21.5	1573	9	BC030199	BC030199 Homo sapi
33	284.2	21.5	8440	9	AF009425	AF009425 Homo sapi
34	281	21.3	8039	9	AF009427	AF009427 Homo sapi
35	250.2	18.9	172692	2	AP001013	AP001013 Homo sapi
36	250.2	18.9	173709	2	AP001010	AP001010 Homo sapi
37	250.2	18.9	181083	2	AP001268	AP001268 Homo sapi
38	240.8	18.2	766	10	BC022716	BC022716 Mus muscu
39	232.6	17.6	240453	2	AC097603	AC097603 Rattus no
40	232.6	17.6	280575	2	AC117364	AC117364 Rattus no
41	231	17.5	183681	2	AC111069	AC111069 Mus muscu
42	222.2	16.8	167489	2	BX005347	BX005347 Danio rer
43	208	15.7	176458	2	AC134911	AC134911 Mus muscu
44	180.8	13.7	155348	5	AL928820	AL928820 Zebrafish
45	128	9.7	175754	2	AC110189	AC110189 Mus muscu

ALIGNMENTS

RESULT 1
LOCUS AX392417 1321 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 1 from Patent WO0216416.
ACCESSION AX392417
VERSION AX392417.1 GI:19700732
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 Lee R.T., Landschulz, K.T., Kennedy, S.P., Thompson, J.F. and
Turi, T.G.
TITLE Diagnosis and treatment of cardiovascular conditions

Pred. No. is the number of results predicted by chance to have a

JOURNAL Patent: NO 0216416-A 1 28-FEB-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; PFIZER INC. (US)

FEATURES
Location/Qualifiers

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/db_xref="taxon:9606"
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/translation="MRLMGVNSTAAAGOPNSCTCNCKRSLFOSMEITELFVQI
IIIVVMYMYVYITCLSHYKLSASFLSRSGRRRDALSSRECLMPSTYSGN
GIDPEVYVAPPRDRLAVPFRQREHFRPPTPYLDLDEIDLPPTISLSGEERP
YQSPCTLOLRDEPQOLELNRESVRAPNRTIFDSLDMLRGLGCPSPNSGISATC
YSGSGMEGPPPTYSYEVIGHYPSFSFOHOSGSPSLBLGTRLHHTHAPLESAAIWS
KERDOKGPHL"

BASE COUNT 223 a 493 c 440 g 165 t

GIN

Very Match 100.0%; Score 1321; DB 6; Length 1321;
Best Local Similarity 100.0%; Pred. No. 1.9e-176;
Matches 1321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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61 CGGCGCGCGCGCGCGCGCGCGCTCGGCTGGGAGAAAGCTAGCGGAGAGCTACGCGCC 120
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301 CTGCG 360
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481 GTGCAACTGCAAAAGCTCTTGTTCAGAGCATGAGATGACGAGAGCTGAGTTGTTC 540
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721 AATCCAGAGCGCGAGGTCTACGCGCGCGCTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
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901 CCGCTGCAACCTTCAGCTTCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
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1141 CTTCCAGACACAGCAGAGAGAGGCG 1200
1201 CACACACATGCG 1260
1201 CACACACATGCG 1260
1261 AGGACACCTCTCTAGAGGCG 1320
1261 AGGACACCTCTCTAGAGGCG 1320
1321 G 1321
1321 G 1321

RESULT 2
AF305616 4839 bp mRNA linear PRI 21-OCT-2001
LOCUS Homo sapiens SNAG1/PMEP1 mRNA, complete cds.
DEFINITION AF305616.1 GI:16303741
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 4839)
Rae,F.K., Hooper,J.D., Nicol,D.L. and Clements,J.A.
Characterization of a novel gene, STAG1/PMEP1, upregulated in
renal cell carcinoma and other solid tumors
Mol. Carcinog. 32 (1), 44-53 (2001)
JOURNAL
MEDLINE
PUBMED
11568975
REFERENCE
2 (bases 1 to 4839)
Rae,F.K., Hooper,J.D., Nicol,D.L. and Clements,J.A.
Direct Submission
Submitted (14-SEP-2000) Centre for Molecular Biotechnology,
Queensland University of Technology, 2 George St, Brisbane, QLD
4001, Australia
FEATURES
source
1. 4839
/organism="Homo sapiens"
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CDS

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YQGRCTQLNDPEQLELNRESTRAPRNRTITFSDLDMSALGCPSPSSGTSATC
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2463..2468
polya_signal
4818..4823
BASE COUNT 1103 a 1313 c 1290 g 1133 t
ORIGIN

Query Match 93.0%; Score 1229; DB 9; Length 4839;
Best Local Similarity 100.0%; Pred. No. 1,3e-163;

Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 GGAAGCTAGCGGAGAGGCTACGCGCGGCGAGCGCGCGCTGCCAGCCATT 152
DB 1 GGAAGCTAGCGGAGAGGCTACGCGCGGCGAGCGCGCGCTGCCAGCCATT 60
QY 153 TTCCGGAGCGCAACCGGGGCGACATGCGGACGCGCGCGGCGCTGCCAGAGGAGCGCGG 212
DB 61 TTCCGGAGCGCAACCGGGGCGACATGCGGACGCGCGCGGCGCTGCCAGAGGAGCGCGG 120
QY 213 GGGGCGAGCGAGCGCGCTCCGCGCACTGAGCCCGCGGCGCGCGCGGAGACTTGGCGGC 272
DB 61 TTCCGGAGCGCAACCGGGGCGACATGCGGACGCGCGCGGCGCTGCCAGAGGAGCGCGG 120
QY 121 GGGGCGAGCGAGCGCGCTCCGCGCACTGAGCCCGCGGCGCGCGGAGACTTGGCGGC 180
DB 273 GACCCGAGCGCGCGAGCGCGCGCGCTCCCGCGCGCGCGCTCCGATGCGGAGCGGC 332
QY 181 GACCCGAGCGCGCGAGCGCGCGCGCTCCCGCGCGCGCGCTCCGATGCGGAGCGGC 240
DB 333 CCCAGCTCCGGGCGCGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 392
QY 241 CCCAGCTCCGGGCGCGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
DB 393 GCCCGCGCGCGCGCGCGCTCATGACGCGCTGATGGGGGTCAACGACCGCGCGCGCG 452
QY 301 GCCCGCGCGCGCGCGCGCTCATGACGCGCTGATGGGGGTCAACGACCGCGCGCGCG 360
DB 453 CCGCGCGCGCGCGCGCAATGCTCTGCGACGCTGCAACTGCAAAAGCTCTTTGTTCCAGACA 512
QY 361 CCGCGCGCGCGCGCGCAATGCTCTGCGACGCTGCAACTGCAAAAGCTCTTTGTTCCAGACA 420
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QY 421 TGGAGATCAGGAGACTGGAGTTGTGTCAGATCATCATATGTTGGTGTGATGAGTGA 480
DB 573 TGGTGTGTGATGATGCTGCTGCTGAGACCACTACAACTGCTGTCAGAGGAGCTTCATCA 632
QY 481 TGGTGTGTGATGATGCTGCTGCTGAGACCACTACAACTGCTGTCAGAGGAGCTTCATCA 540
DB 633 GCCGCGACAGCCAGGGGCGGAGAGAGAAATGCGCTGCTCTCAGAAAGATGCGCTGGC 692
QY 541 GCCGCGACAGCCAGGGGCGGAGAGAGAAATGCGCTGCTCTCAGAAAGATGCGCTGGC 600
DB 693 CCTGGAGAGACAGTGTACAGCAAGCAATCCAGAGCGGAGTCTACGCGCGCGCTC 752
QY 601 CCTGGAGAGACAGTGTACAGCAAGCAATCCAGAGCGGAGTCTACGCGCGCGCTC 660
DB 753 GGGCCACGACGCGCTGCGCGCTGCGCGCTGCGCGCGGAGGCGCTTCACGCGCTTC 812
QY 661 GGGCCACGACGCGCTGCGCGCTGCGCGCTGCGCGCGGAGGCGCTTCACGCGCTTC 720

QY 813 AGCCACCTATCCGTAAGCTGACAGCAGAGATGACGACCTGACACCAACATCTGCTGTCAG 872
DB 721 AGCCACCTATCCGTAAGCTGACAGCAGAGATGACGACCTGACACCAACATCTGCTGTCAG 780
QY 873 ACGGGGAGGAGACCCCAACCTTACAGAGGCGCCCTGACCTTCAGCTTGGGAGCCCGAGC 932
DB 781 ACGGGGAGGAGACCCCAACCTTACAGAGGCGCCCTGACCTTCAGCTTGGGAGCCCGAGC 840
QY 933 AGCAGCTGGAAGTGAACCGGGAGTGGTGGCGGACCGCCCAAGAGCAACATCTTCGACA 992
DB 841 AGCAGCTGGAAGTGAACCGGGAGTGGTGGCGGACCGCCCAAGAGCAACATCTTCGACA 900
QY 993 GTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1052
DB 901 GTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
QY 1053 TCAGCGCGCAGCTGCTACGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1112
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QY 1113 AGTTCATGCGGCGACCTACCGGGGCTCTCTTCAGACACAGCAGAGAGAGAGAGAGAGAG 1172
DB 1021 AGTTCATGCGGCGACCTACCGGGGCTCTCTTCAGACACAGCAGAGAGAGAGAGAGAG 1080
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QY 1233 TCTGAGCAAGAGAGAGATTAACAGAAAGAGACACCTCTTAGGGTCCCAAGGGGGCC 1292
DB 1141 TCTGAGCAAGAGAGAGATTAACAGAAAGAGACACCTCTTAGGGTCCCAAGGGGGCC 1200
QY 1293 GGGCTGGGGCTGCGTAGGTGAAAGAGCAG 1321
DB 1201 GGGCTGGGGCTGCGTAGGTGAAAGAGCAG 1229

RESULT 3
BC015918
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1061)
Strausberg, R.
Direct Submission
Submitted (15-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-7590,
USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DP
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (TLNL)
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca

REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK
COMMENT

Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Kizylinski, Reta Kusche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabh, Parvaneh Seedei, Jacqueline
Schein, Diane Smilans, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Db 617 CAGTAATCTGGGATCAGCGCCACACTGCTACGCGAGCGGGCGCATGAGAGGCGCC 676

OY 1099 GCCCACTACAGCAGAGGTGATCGGCGCACTACCGGGGTCTCTCTCCAGCAGCAGCAG 1158

Db 677 GCCCACTACAGCAGAGGTGATCGGCGCACTACCGGGGTCTCTCTCCAGCAGCAGCAG 736

OY 1159 CAGTGGGCGGCGCT 1218

Db 737 CAGTGGGCGGCGCT 796

OY 1219 AGAGAGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1278

Db 797 AGAGAGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 856

OY 1279 TCCCCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1321

Db 857 TCCCCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 899

RESULT 6
US 18643

DEFINITION Homo sapiens PMPAL variant A protein mRNA, complete cds.
ACCESSION AY128643
VERSION AY128643.1 GI:22121998

KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

1 (bases 1 to 1818)
Brunschwig, E.B., Wilson, K., Mack, D., Dawson, D., Lawrence, E.,
Willison, J.K., Lu, S., Nosrati, A., Retko, R.M., Swidler, S., Beard, L.,
Luttrebaugh, J.D., Willis, J., Platzer, P. and Markowitz, S.
PMPAL, a transforming growth factor-beta-induced marker of
terminal colonocyte differentiation whose expression is maintained
in primary and metastatic colon cancer
Cancer Res. 63 (7), 1568-1575 (2003)

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

JRNS
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1. 1818
/organism="Homo sapiens"
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BASE COUNT 459 a 467 c 494 g 398 t

ORIGIN
Query Match 60.6%; Score 800; DB 9; Length 1818;
Best Local Similarity 100.0%; Pred. No. 3.1e-103;
Matches 800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 522 CGGAGCTGAGCTTTGTCAGATCATCATCGTGTGTGAGTANGATGATGTGTG 581

Db 104 CGGAGCTGAGCTTTGTCAGATCATCATCGTGTGTGAGTANGATGATGTGTG 163

OY 582 TGATCAAGTCTCTGTAGAGCAGTACAGTCTCTGACAGGTCTTTATCAGCGGCA 641

Db 164 TGATCAAGTCTCTGTAGAGCAGTACAGTCTCTGACAGGTCTTTATCAGCGGCA 223

OY 642 GCCAGGGGCGAG 701

Db 224 GCCAGGGGCGAG 283

OY 702 GCACAGTGTAG 761

Db 284 GCACAGTGTAG 343

OY 762 AGCGCTGGCGGCT 821

Db 344 AGCGCTGGCGGCT 403

OY 822 ATCCGTACCTGACAGAGATGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 881

Db 404 ATCCGTACCTGACAGAGATGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 463

OY 882 AGCCCCACCTTACAGAGGCGGCTCTGACAGCTCTGAGAGAGAGAGAGAGAGAGAG 941

Db 464 AGCCCCACCTTACAGAGGCGGCTCTGACAGCTCTGAGAGAGAGAGAGAGAGAGAG 523

OY 942 AACAGACCGGAGTGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1001

Db 524 AACAGACCGGAGTGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 583

OY 1002 TGGATAGTCCAGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1061

Db 584 TGGATAGTCCAGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 643

OY 1062 CGGTGACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1121

Db 644 CGGTGACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 703

OY 1122 GCCACTACCGGCGGCT 1181

Db 704 GCCACTACCGGCGGCT 763

OY 1182 AGGGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1241

Db 764 AGGGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 823

OY 1242 AAGAGAGGATTAACAGAAAGACACCTCTCTAGAGTCCCAAGGGGGCGGCGTGGG 1301

Db 824 AAGAGAGGATTAACAGAAAGACACCTCTCTAGAGTCCCAAGGGGGCGGCGTGGG 883

OY 1302 CTGCGTAGGTGAAGAAGCGAG 1321

Db 884 CTGCGTAGGTGAAGAAGCGAG 903

RESULT 7
LOCUS BC036995 1379 bp mRNA linear ROD 26-SEP-2002
DEFINITION Mus musculus, similar to transmembrane, prostate androgen induced
RNA, clone IMAGE:5038092, mRNA.
ACCESSION BC036995
VERSION BC036995.1 GI:23331176
KEYWORDS
SOURCE Mus musculus (house mouse)

ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1379)
Straussberg, R.
Direct Submission
Submitted (23-AUG-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer

REMARK
COMMENT
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk

Tissue Procurement: Gilbert Smith, Ph.D.
 Tissue Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNI)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>

Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgcen@nrl.nih.gov
Akhter, N., Ayele, K., Beckstrom-Stenberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.C., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-l., Karlins, E., Kwong, P., Latic, P., Legaspi, R., Maduro, O.L., Mastillo, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, C., Pearson, R., Stantirup, S., Thomas, P.J., Touchman, J.W., Young, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAG Plate: 81 Row: 1 Column: 11
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

FEATURES

source

Location/Qualifiers
1. .1379

Db 769 AACGGG

[illegible]

CTCGCACATGCCCCACTG 828

ORIGIN

Query Match 46.7%; Score 616.4; DB 6; Length 878;
 Best Local Similarity 84.3%; Pred. No. 2,2e-77;
 Matches 740; Conservative 0; Mismatches 111; Indels 27; Gaps 3;

416 CACCGCTGATGGGGGTCACAGCAGCCGCCGCCGCCGCCGCCGCCGCCCAATGTCAC 475
 11 CAGGCTTGATGGGGGTCACAGCAGCCGCCGCCGCCGCCGCCGCCCAATGTCAC 70

476 TGCAGCTGCAATGCAAGACCTCTTGTTCAGACATGAGATGAGATGAGATGAGAT 535
 71 TGCAGCTGCAATGCAAGACCTCTTGTTCAGACATGAGATGAGATGAGATGAGAT 130

536 GTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 595
 131 GTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 190

596 CTGAGCCACTACAGATGATGATGATGATGATGATGATGATGATGATGATGATG 655
 191 CTGAGCCACTACAGATGATGATGATGATGATGATGATGATGATGATGATGATG 250

656 AGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 715
 251 AGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 309

716 AACGGAATCCAGAGCCGAGGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 775
 310 --TGAATGCGGAGCCAGAGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 367

776 CCGCCTTCCGCGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 835
 368 CCGCCTTCCGCGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 418

836 CAGAGATGACCTGCAACCCACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 895
 419 CAGAGATGACCTGCAACCCACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 478

896 CAGGCGCTGCAACCCACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 955
 479 CAGGCGCTGCAACCCACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 538

956 TCGTGCAGCAGCCCAACCAAGACCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1015
 539 TCGTGCAGCAGCCCAACCAAGACCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 598

1016 CTGGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1075
 599 CTGGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 658

1076 GGGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1135
 659 GGGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 718

1136 TCGTGCAGCAGCCCAACCAAGACCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1195
 719 TCGTGCAGCAGCCCAACCAAGACCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 778

1196 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1255
 779 CATGACTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 823

1256 CAGAAAGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1293
 824 CAGAAAGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 861

RESULT 9
 AF305426 61505 bp DNA linear PRI 12-OCT-2001
 LOCUS Homo sapiens solid tumor-associated 1 protein (STAG1/PMEP1) gene,
 complete cds.
 ACCESSION AF305426

VERSION
KEYWORDS
SOURCE
ORGANISM

AF305426.1 GI:15824468
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 61505)
 Rae, F.K., Hooper, J.D., Nicol, D.L. and Clements, J.A.
 Identification and characterization of a novel gene, STAG1,
 up-regulated in renal cell carcinoma and other solid tumours

JOURNAL

Unpublished
 2 (bases 1 to 61505)
 Rae, F.K., Hooper, J.D., Nicol, D.L. and Clements, J.A.

AUTHORS

Submitted (13-SEP-2000) Centre for Molecular Biotechnology,
 Queensland University of Technology, 2 George St, Brisbane, QLD
 4001, Australia

FEATURES

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 GIEPEQVAVPPEPTDLAVPFAQEREREPYVYQHEIDPPTLSLSDGEPP
 YGSPNCLQIARPEQDLNRESVRAVPNTIFDSLDMSARVAGCPSPSSGASATC
 YSGGMEGRPPPTYSVHYGHYRPGSSPHQSSGPPSLLEGTRHHTHIAPLESAIWS
 KENDKONGHPL"

BASE COUNT

13329 a 16074 c 17430 g 14672 t

ORIGIN

Query Match 45.0%; Score 594.4; DB 9; Length 61505;
 Best Local Similarity 99.0%; Pred. No. 1.3e-74;
 Matches 598; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

718 CGGAATCCAGAGCCGAGGTCTACGCCGCCGCTCGGCCACGACGCGCTGGCGTGC 777
 57292 CTGCTTCCTCCAGCGCGAGGTCTACGCCGCCGCTCGGCCACGACGCGCTGGCGTGC 57351

778 GCCCTGGCCAGGGAGGCGCTTCCACCGCTTCCAGCCCACTATCCGTACTGCAGCA 837
 57352 GCCCTGGCCAGGGAGGCGCTTCCACCGCTTCCAGCCCACTATCCGTACTGCAGCA 57411

838 CGAGATGACCTGCAACCCACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 897
 57412 CGAGATGACCTGCAACCCACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 57471

898 GGGCCCTGCAACCCCTCCAGCTTGGGAGCCCGAGACACACACTGGAATGAAACGGGAGTC 957
 57472 GGGCCCTGCAACCCCTCCAGCTTGGGAGCCCGAGAGACACACTGGAATGAAACGGGAGTC 57531

958 GGTGGCGCACCCCAACAGAACCATCTTGCAGAGTACCTGATGATGATGATGATGATG 1017
 57532 GGTGGCGCACCCCAACAGAACCATCTTGCAGAGTACCTGATGATGATGATGATGATG 57591

1018 GGGGGCGCCCTGCCCCCAGCAGTAACTCGGGGATCAGCGCGCAGTACCGGACGCG 1077
 57592 GGGGGCGCCCTGCCCCCAGCAGTAACTCGGGGATCAGCGCGCAGTACCGGACGCG 57651

1078 CGGGGCAATGAGGGGCGCGCCCACTACAGGAGGTCACTGCGCCACTACCGGGGTC 1137

DB 57652 CGGGCGCATGGAGGGGCGCGCCGACCTACAGCGAGGTCACTACCGCGGGTCC 57711
 OY 1138 CTCTCTTCAGACACGACGAGAGAGTGGGCGCCCTCTTGTGAGGGGAGCCGGCTCCA 1197
 DB 57712 CTCTCTTCAGACACGACGAGAGAGTGGGCGCCCTCTTGTGAGGGGAGCCGGCTCCA 57711
 OY 1198 CCACACACATCGGCGCCCTAGAGAGCGCACCATCTGTGAGCAAGAAGATTAACA 1257
 DB 57772 CCACACACATCGGCGCCCTAGAGAGCGCACCATCTGTGAGCAAGAAGATTAACA 57831
 OY 1258 GAAAGACACCTCTCTAGAGTGGGCGCGCGCTGGGGCTCCGTAGCTAAGAAG 1317
 DB 57832 GAAAGACACCTCTCTAGAGTGGGCGCGCGCTGGGGCTCCGTAGCTAAGAAG 57891
 OY 1318 GCAG 1321
 DB 57892 GCAG 57895

PLN 10
 1837/c

DEFINITION HS718J7 130435 bp DNA linear PRI 24-FEB-2001
 LOCUS Human DNA sequence from clone RP4-718J7 on chromosome 20q13.31-13.33 contains the PKI gene for soluble

phosphoenolpyruvate carboxylase 1, part of a novel gene similar to mouse DLM-1 (tumour stroma and activated macrophage protein), the 3' end of the TMEM41 gene encoding an androgen induced 1b transmembrane protein (PMEPA1), two putative novel genes, a Cps 1sland, ESTs, STSs and GSSs, complete sequence.

ACCESSION AL035541.15 GI:11546043
 VERSION HTG; Cpg Island; DLM-1; macrophage protein; PKI;
 KEYWORDS phosphoenolpyruvate carboxylase; PMEPA1; TMEM41; transmembrane

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 TITLE 1 (bases 1 to 130435)
 JOURNAL Sehara, H.

COMMENT Direct Submission
 Submitted (23-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
 requests: clonerequest@sanger.ac.uk
 On Dec 5, 2000 this sequence version replaced gi:10198628.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WormPeP; Information on the WormPeP database can be found at

http://www.sanger.ac.uk/projects/C-elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20

Mapping Group. Further information can be found at

http://www.sanger.ac.uk/HGP/Chr20

This sequence is the entire insert of clone RP4-718J7 The true left end of clone RP5-1007E6 is at 71437 in this sequence. The true

right end of clone RP4-579F20 is at 43945 in this sequence. RP4-718J7 is from the library RPCI-4 constructed by the group of

Pieter de Jong. For further details see

http://www.choi1.org/bacpac/home.htm

VECTOR: pCYPAC2

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least

FEATURES
 source one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

1. 130435
 /organism="Homo sapiens"
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 3799. .3896
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 6952. .7021
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 7358. .7671
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 8521. .8554
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 8863. .9217
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 9880. .10089
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 10094. .10206
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QY	778	GCCCTTCCGAGGCGGAGGCTTCCACGCGCTTCCAGCCACCTATCCGTACTTGACGA	837		
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QY	838	CGAGATCGACCTGCCACCCACCATCTGCTGTGAGAGGGGAGGAGGCCGCCACCTACCA	897		
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QY	898	GGGCGCCGACCCGCTCCAGCTTGGGAGCCCGGAGCAGCAGCTGGAACCTGACCGGAGTC	957		
Db	128274	GGGCGCCGACCCGCTCCAGCTTGGGAGCCCGGAGCAGCAGCTGGAACCTGACCGGAGTC	128215		
QY	958	GGTGGCGGACCCCAAGACACATCTTGCACAGTACGTATGATGATAGTCCAGGCT	1017		
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QY	1018	GGGCGGCGCCCTGCGCCCGCCAGCAGTAACTCGGGCATCAGCGCCAGCTGCTACGGCAGCG	1077		
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QY	1078	CGGGCGCATGAGAGGGGCGCGCCACCTAAGAGGAGGTATGCGGCACACCGGGGTC	1137		
Db	128094	CGGGCGCATGAGAGGGGCGCGCCACCTAAGAGGAGGTATGCGGCACACCGGGGTC	128035		
QY	1138	CTGCTTCCAGCAGCAGCAGAGCAGTGGGGCGCCCTCTGCTGAGGGAGCCCGCTCCA	1197		
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QY	1198	CCACACACACATCGGGCCCTAGAGAGGGGAGCCATCGGAGCAGCAAGAGGATAAACA	1257		
Db	127974	CCACACACACATCGGGCCCTAGAGAGGGGAGCCATCGGAGCAGCAAGAGGATAAACA	127915		
QY	1258	GAAAGGACACACCTCTTAGGGTCCCGAGGGGGCGGGGCTGGGCTCGTAGGTGAAGAAG	1317		
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QY	1318	GCAG 1321			
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DEFINITION	Sequence 32 from Patent WO0242776.				
ACCESSION	AX593655				
VERSION	AX593655.1	GI:28375034			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE					
AUTHORS	Sun,Y., Recipon,H., Chen,S.Y. and Liu,C.				
TITLE	Compositions and methods relating to prostate specific genes and proteins				
JOURNAL	Patent: WO 0242776-A 32 30-MAY-2002;				
FEATURES	Diadexis, Inc. (US)				
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DB 52656	TGAGCCCCGGGGCCCCCGGAACTTGGCGGCGAACCCGAGCCCGGGGAGACCGGGCGGCG 52597
QY 301	CTCCCGCGCGCGGCTCTGCTGCAATGGGGGGGCCCAAGCTCCGAGGCCCGCGGAGAGCCG 360
DB 52596	CTCCCGCGCGCGGCTCTGCTGCAATGGGGGGGCCCAAGCTCCGAGGCCCGGGGAGAGCCG 52537
QY 361	CCCGGCGCGCCCCCGGAGCCCCCGCGCCGCGCGCGCGCGCGCGCGCTGCATGCAACCG 420
DB 52536	CCCGGCGCGCCCCCGGAGCCCCCGCGCCGCGCGCGCGCGCGCGCGCTGCATGCAACCG 52477
QY 421	CTGATGGGGGTCAACGCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCAATGTCCTCGAC 480
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△

RESULT 13
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 LOCUS
 DEFINITION
 AX392430
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AX392430
 Sequence 14 from Patent W00216416.
 AX392430
 AX392430.1 GI:19700746
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1
 Lee, R.T., Landschulz, K.T., Kennedy, S.P., Thompson, J.F. and
 Turi, T.G.
 Diagnosis and treatment of cardiovascular conditions
 Patent: WO 0216416-A 14 28-FEB-2002;
 THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; PFIZER INC. (US)

TITLE
 JOURNAL
 THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; PFIZER INC. (US)

FEATURES
 source
 1. .693
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ORIGIN

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 D 633 CACGAGATCGA-CGCGCGCCGACCATCTCGCTGCAGCGGAG--AGGAGCCGCCACCTAC 577
 QY 896 CAGGCGCCCTGCACCTTCACCTTCGCGGAGCCCGAGCAGCAGCTGGAAGTGAACCGGGAG 955
 D 576 CAGGCGCCCTGCACCTTCACCTTCGCGGAGCCCGAGCAGCAGCTGGAAGTGAACCGGGAG 517
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 QY 1076 GCGCGCGCATGAGAGGCGCGCGCCGACCTACAGCAGGATCGAGGCGCATACCGGGG 1135
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 QY 1195 CCACACACACATCGGCGCCCTTAGAGAGCGCAGCCATCTGGAGCAAGAGAGATTA 1254
 D 276 CCGCCACACACATCGGCGCCCTTAGAGAGCGCAGCCATCTGGAGCAAGAGAGATTA 217
 QY 1255 ACAGAAAGGACACCTCTCTAGGGTCCCGAGGGGGCGGGGCTGGGGTGGGTAGGTAA 1314
 D 216 ACAGAAAGGACACCTCTCTAGGGTCCCGAGGGGGCGGGGCTGGGGTGGGTAGGTAA 157
 QY 1315 AAGGAG 1321
 D 156 AAGGAG 150

AF220208
 LOCUS
 DEFINITION
 AF220208
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AF220208
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 AF220208
 AF220208.1 GI:12004973
 Mus musculus
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Scurionath; Muridae; Murine; Mus.

REFERENCE
 1
 Jolliffe, C.N., Harvey, K.F., Haines, B.P., Parasiyam, G. and Kumar, S.
 Identification of multiple proteins expressed in murine embryos as
 binding partners for the WW domains of the ubiquitin-protein ligase
 Nedd4
 Blochem. J. 351 Pt 3, 557-565 (2000)

JOURNAL
 MEDLINE
 PUBMED
 11042109
 2 (bases 1 to 651)
 Jolliffe, C.N. and Kumar, S.
 Direct Submission
 Submitted (30-DEC-1999) Division of Haematology, Hanson Centre for
 Cancer Research, IMVS, Frome Rd, Adelaide, SA 5000, Australia

TITLE
 JOURNAL
 Cancer Research, IMVS, Frome Rd, Adelaide, SA 5000, Australia

FEATURES
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ORIGIN

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 D 61 AGTACGGGTGTAGG---TGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 117
 QY 761 GACCGCTGTGCG 820
 D 118 GACCGCTGTGCG 168
 QY 821 TATCGGTACCTGTGAGCAGAGATGAGTGTGCGACCCACCATCTGCTGTGAGCGGAG 880
 D 169 TACCGGTACCTGTGAGCAGAGATGAGTGTGCGACCCACCATCTGCTGTGAGCGGAG 228
 QY 881 GAGCG 940
 D 229 GAGCG 288
 QY 941 GAATGTGAACCGGAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1000
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 QY 1181 GAGGGAGCGGGGGTCCACACACACATCGCGCCCTAGAGAGGCGAGCCATCTGGAGC 1240
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 Db 574 AAGAGAGAGATTAACAGAAAGAGTCAACCCCTTAG 610

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 AX011709 812 bp DNA linear PAT 06-SEP-2000
 DEFINITION Sequence 107 from Patent W0955858.
 ACCESSION AX011709
 VERSION AX011709.1 GI:9998233
 KEYWORDS
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 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 Patent: WO 9955858-A 107 04-NOV-1999;
 SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
 BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN
 (DE); PILARSKY CHRISTIAN (DE)

FEATURES

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Search completed: August 27, 2003, 19:16:51
 Job time : 5036 secs

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OY	1201	CACACACATCGCGCCCTTAGAGAGCGCAGCCATCTTGAGCAAAAGAAAGATTAACAGAA	1260
Db	1201	CACACACATCGCGCCCTTAGAGAGCGCAGCCATCTTGAGCAAAAGAAAGATTAACAGAA	1260
OY	1261	AGGACACCCCTCTTAGAGGTCCCGAGGGGGGCGGGCTGGGGGTGCGTAGTGAAGAAAGCA	1320
Db	1261	AGGACACCCCTCTTAGAGGTCCCGAGGGGGGCGGGCTGGGGGTGCGTAGTGAAGAAAGCA	1320
OY	1321	G 1321	
Db	1321	G 1321	
RESULT 2			
ID AAA75151 standard; cDNA: 969 BP.			
AC AAA75151;			
XX 15-JAN-2001 (first entry)			
DE cDNA encoding a human TANGO 261 polypeptide.			
XX TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267;			
KW cellular proliferation; cellular differentiation; cellular adhesion;			
KW von Willebrand factor-associated disorder; cell trafficking; cancer;			
KW hemiplolethal associated disease; atelectasis; pulmonary congestion;			
KW oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;			

XX	Homo sapiens.
OS	
XX	
XX	Intestinal disorder; spleen associated disease; renal disorder;
KW	cardiovascular disorder; ischemic heart disease; hydrocephalus;
KM	brain herniation; iatrogenic disease; inflammation; meningitis;
KM	Alzheimer's disease; cerebral toxoplasmosis; Parkinson's disease;
XX	multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
XX	
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	6..764
FT	/tag= a
FT	/product= "TANGO 261"
FT	sig_peptide
FT	6..89
FT	/tag= b
FT	mat_peptide
FT	90..764
XX	/tag= c
XX	
PN	MO200052022-A1.
XX	
XX	08-SEP-2000.
PR	01-MAR-2000; 2000WO-USO5226.
PA	01-MAR-1999; 99US-0122458.
PI	(MILL-) MILLENNIUM PHARM INC.
PB	Barnes TM, Holtzman DA, Sharp JD, Fraser CC;
DR	WPJ: 2000-579269/54.
XX	P-PSDB; AAB18449.
PT	Novel human and murine secreted proteins designated TANGO 216, 261,
PT	262, 266 and 267 useful as modulating agents of cellular processes,
PT	e.g. for treating cancer -
XX	
XX	Claim 2; Fig 5; 175pp; English.
XX	
CC	The present sequence encodes a human TANGO 261 polypeptide. The
CC	specification also describes TANGO 266, TANGO 216, TANGO 262, and
CC	TANGO 267. The TANGO polypeptides can be used to modulate cellular
CC	proliferation, modulate cellular differentiation and/or modulate
CC	cellular adhesion. The proteins can be used to treat any von Willebrand
CC	factor-associated disorder, regulate extracellular matrix structuring,
CC	cellular adhesion, and cell trafficking and/or migration, modulate
CC	cellular interactions, modulate cell adhesion in proliferative
CC	disorders, such as cancer, modulate the proliferation, differentiation,
CC	and/or function of cells that appear in the bone marrow, and leukocytes,
CC	treat bone marrow, blood and hematopoietic associated diseases and
CC	disorders; atelectasis, pulmonary congestion or edema, emphysema,
CC	chronic bronchitis, bronchial asthma and bronchiectasis, intestinal
CC	disorders, spleen associated diseases, modulate renal disorders, treat
CC	cardiovascular disorders such as ischemic heart disease, modulate the
CC	proliferation, differentiation, and/or function of bone and cartilage
CC	cells and to treat bone and/or cartilage associated diseases or
CC	disorder. They may also be used to treat disorders associated with the
CC	ovaries, cerebral edema, hydrocephalus, brain herniations, iatrogenic
CC	disease, inflammations, bacterial and viral meningitis, Alzheimer's
CC	disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis,
CC	brain cancers, hydrocephalus and encephalitis, and treat hepatic
CC	disorders.
SQ	
XX	Sequence 969 BP; 211 A; 316 C; 294 G; 148 T; 0 other;
Query Match	60.8%; Score 803.2; DB 21; Length 969;
Best Local Similarity	99.6%; Pred. No. 1,9e+120;
Matches 805; Conservative	0; Mismatches 3; Indels 0; Gaps 0
OY	514 GGAGATCACGCGAGCTGGATTGTTCAGATCATCATCATCGTGTCGATGATGTGAT 573 db 2 GGAGATGCGCGAGCTGGATTGTTCAGATCATCATCATCGTGTCGATGATGTGAT 61
OY	574 GTGTGTGTGATCACGCTCTGTGAGCACTAACAAGCTGTGTGCAGCGTCTTCATCAG 633

Db	62	GGTGGTGGTATCATCGTGCCTGCTGAGCCACTACAGCTGTCTGACGGTCTTTCATCAG	121
QY	634	CCGGCACAGCCAGGGGGGAGAGAGAAGATGCCCTGTCTCTCAGAAAGATGCCCTGTGGCC	693
Db	122	CCGGCACAGCCAGGGGGGAGAGAGAAGAAGATGCCCTGTCTCTCAGAAAGATGCCCTGTGGCC	181
QY	694	CTCGGAGAGCACAATGTCTCAGGCAACGGAAATCCAGAGCCGGAGGTCTTACGCCCGCTCG	753
Db	182	CTCGGAGAGCACAATGTCTCAGGCAACGGAAATCCAGAGCCGGAGGTCTTACGCCCGCTCG	241
QY	754	GCCCAACGACCGACCTGGGCGTGGCGCCCTTGGCCAGGGGAGGGGCTTCCACGCGCTTCCA	813
Db	242	GCCCAACGACCGCGCTTGGCGCGTGGCGCCCTTGGCCAGGGGAGGGGCTTCCACGCGCTTCCA	301
QY	814	GCCCAACCTATCCGTACCTGACAGCAAGATGCAGCTGGCACCCACCAATCTTGTGTGAGA	873
Db	302	GCCCAACCTATCCGTACCTGACAGCAAGATGCAGCTGGCACCCACCAATCTTGTGTGAGA	361
QY	874	CGGGGAGAGAGCCCGACCCCTACACAGAGGCCCTGCAACCTCTCCAGTTGGGGACCCCGAGCA	933
Db	362	CGGGGAGAGAGAGCCCGACCCCTACACAGAGGCCCTGCAACCTCTCCAGTTGGGGACCCCGAGCA	421
QY	934	GCACCTGGAACTGAACCGGGGAGTGGGTGGCGGACCCCGCAACAGAACATCTTCGACAG	993
Db	422	GCACCTGGAACTGAACCGGGGAGTGGGTGGCGGACCCCGCAACAGAACATCTTCGACAG	481
QY	994	TGACCTGATGATATGATGCTCCAGGCTGGGGGCGCCCTGCGCCCGCCAGCAAGTAACTGGGCAT	1053
Db	482	TGACCTGATGATATGATGCTCCAGGCTGGGGGCGCCCTGCGCCCGCCAGCAAGTAACTGGGCAT	541
QY	1054	CAGCGCCACAGCTGTACAGGCAAGCGGCGGGCGCATGAGAGGGGCGCGCCCGCCACTTACAGCA	1113
Db	542	CAGCGCCACAGCTGTACAGGCAAGCGGCGGGCGCATGAGAGGGGCGCGCCCGCCACTTACAGCA	601
QY	1114	GGTCATGGGCGCACTACCCGGGGGTCTCTCTTCACACACAGAGAGAGAGTGGGGCGCCCTC	1173
Db	602	GGTCATGGGCGCACTACCCGGGGGTCTCTCTTCACACACAGAGAGAGAGTGGGGCGCCCTC	661
QY	1174	CTTGTCTGAGGGGACCCGGGCTCCACACACACACATGCGGCCCTAGAGAGCGCAGCCAT	1233
Db	662	CTTGTCTGAGGGGACCCGGGCTCCACACACACACATGCGGCCCTAGAGAGCGCAGCCAT	721
QY	1234	CTGAGAGCAAGAGAGATTAACAGAAAGACACCCCTCTCTAGGGTCCCGCAGGGGGGCGCG	1293
Db	722	CTGAGAGCAAGAGAGATTAACAGAAAGACACCCCTCTCTAGGGTCCCGCAGGGGGGCGCG	781
QY	1294	GGCTGGGGGCTGCTAGGTGTAAGAAAGGCAAG	1321
Db	782	GGCTGGGGGCTGCTAGGTGTAAGAAAGGCAAG	809
RESULT 3			
ABK92120			
ID ABR92120 standard; DNA; 1140 BP.			
XX	AC	ABK92120;	
XX	AC	(ABK92120;	
XX	AC	15-AUG-2002 (first entry)	
XX	AC	Prostate cancer-associated DNA sequence #6.	
XX	AC	Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;	
XX	AC	gene therapy; gene; ds.	
XX	AC	Mammalia.	
XX	AC	OS	
XX	AC	WO200230268-A2.	
XX	AC	18-APR-2002.	
XX	AC	12-OCT-2001; 2001WO-US32045.	

CC AAA75163-65 encode human TANGO 261 proteins. The specification also
 CC describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO
 CC polypeptides can be used to modulate cellular proliferation, modulate
 CC cellular differentiation and/or modulate cellular adhesion. The
 CC proteins can be used to treat any von Willebrand factor-associated
 CC disorder, regulate extracellular matrix structuring, cellular adhesion,
 CC and cell trafficking and/or migration, modulate cellular interactions,
 CC modulate cell adhesion in proliferative disorders, such as cancer,
 CC modulate the proliferation, differentiation, and/or function of cells
 CC that appear in the bone marrow, and leukocytes, treat bone marrow, blood
 CC and hematopoietic associated diseases and disorders, osteoarthritis,
 CC pulmonary congestion or edema, emphysema, chronic bronchitis, bronchial
 CC asthma and bronchiectasis, intestinal disorders, spleen associated
 CC diseases, modulate renal disorders, treat cardiovascular disorders such
 CC as ischemic heart disease, modulate the proliferation, differentiation,
 CC and/or function of bone and cartilage cells and to treat bone and/or
 CC cartilage associated diseases or disorder. They may also be used to
 CC treat disorders associated with the ovaries, and cerebral edema,
 CC hydrocephalus, brain herniations, latrogenic disease, inflammation,
 CC bacterial and viral meningitis, Alzheimer's disease, cerebral
 CC toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers,
 CC hydrocephalus and encephalitis, and treat hepatic disorders.
 CC note: the present sequence does not appear in the specification; it was
 CC created using information provided.

XX Sequence 969 BP; 210 A; 317 C; 294 G; 148 T; 0 other:

Query Match 60.7%; Score 801.6; DB 21; Length 969;
 Best Local Similarity 99.5%; Pred. No. 3.3e-120;
 Matches 804; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

514 GGAGATCAGGAGGCTGGAGTTGTTTCAGATCATCATGCTGGTGGTGGATGATGATGAT 573
 2 GGAGATGCGGAGCTGGAGTTGTTTCAGATCATCATGCTGGTGGTGGATGATGATGAT 61
 574 GGTGGTGGTGGATCAGCTGCTGTCAGAGCCATCAAGCTGTCAGAGCTGTCATCAG 633
 62 GGTGGTGGTGGATCAGCTGCTGTCAGAGCCATCAAGCTGTCAGAGCTGTCATCAG 121
 634 CCGGACAGGAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 693
 122 CCGGACAGGAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 181
 694 CTCGAGAGACACAGTGTGAGGCAACGAGATCCAGAGAGGCTGTAAGCCCGCTCG 753
 182 CTCGAGAGACACAGTGTGAGGCAACGAGATCCAGAGAGGCTGTAAGCCCGCTCG 241
 754 GCCCACCAGAGGCTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 813
 242 GCCCACCAGAGGCTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 301
 814 GCCCACCAGAGGCTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 873
 302 GCCCACCAGAGGCTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 361
 874 CCGGAG 933
 362 CCGGAG 421
 934 GGAGCGGAAGTGAACCGGAGAGTGGTGGGCGCAGCCCAACAGAACATCTTGAGAG 993
 422 GGAGCGGAAGTGAACCGGAGAGTGGTGGGCGCAGCCCAACAGAACATCTTGAGAG 481
 994 TGACCTGATGATAGTCCAGAGGCTGGGCGGCTGCTGCCCCCAGACAGTACTCGGGCAT 1053
 482 TGACCTGATGATAGTCCAGAGGCTGGGCGGCTGCTGCCCCCAGACAGTACTCGGGCAT 541
 1054 CAGCGCCACAGTGTGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1113
 542 CAGCGCCACAGTGTGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 601
 1114 GGTCATGGGACATACCGGGGCTCTTCCAGACACAGAGAGAGAGAGAGAGAGAGAGAG 1173

Db 602 GGTCATGGGACATACCGGGGCTCTTCCAGACACAGAGAGAGAGAGAGAGAGAGAG 661
 QY 1174 CTGCTGGAGAGGAG 1233
 Db 662 CTGCTGGAGAGGAG 721
 QY 1234 CTGAGCAAAAGAGAGATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1293
 Db 722 CTGAGCAAAAGAGAGATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 781
 QY 1294 GGCTGGGCTGCTGCTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1321
 Db 782 GGCTGGGCTGCTGCTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 809

RESULT 6

AAA75165
 ID AAA75165 standard; cDNA; 969 BP.

AAA75165;

15-JUN-2001 (first entry)

cDNA clone encoding a human TANGO 261 polypeptide.

TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267;
 cellular proliferation; cellular differentiation; cellular adhesion;
 von Willebrand factor-associated disorder; cell trafficking; cancer;
 hematopoietic associated disease; atelectasis; pulmonary congestion;
 edema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
 intestinal disorder; spleen associated disease; renal disorder;
 cardiovascular disorder; ischemic heart disease; hydrocephalus;
 brain herniation; latrogenic disease; inflammation; meningitis;
 Alzheimer's disease; cerebral toxoplasmosis; Parkinson's disease;
 multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 6..764

XX FT /product- "TANGO 261"

XX WO200052022-A1.

XX 08-SEP-2000.

XX 01-MAR-2000; 2000WO-US05226.

XX 01-MAR-1999; 99US-0122458.

XX (MILL-) MILLENNIUM PHARM INC.

XX Barnes TM, Holtzman DA, Sharp JD, Fraser CC;

XX WPI; 2000-579269/54.

XX P-PSDB; AAB18463.

XX Novel human and murine secreted proteins designated TANGO 216, 261,
 262, 266 and 267 useful as modulating agents of cellular processes,
 e.g. for treating cancer -

XX Disclosure; Page -; 175pp; English.

XX AAA75163-65 encode human TANGO 261 proteins. The specification also
 CC describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO
 CC polypeptides can be used to modulate cellular proliferation, modulate
 CC cellular differentiation and/or modulate cellular adhesion. The
 CC proteins can be used to treat any von Willebrand factor-associated
 CC disorder, regulate extracellular matrix structuring, cellular adhesion,
 CC and cell trafficking and/or migration, modulate cellular interactions,
 CC modulate the proliferation, differentiation, and/or function of cells

(e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's disease), neurological disorders (e.g. epilepsy, Huntington's disease, dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease, multiple sclerosis, cerebral palsy, Parkinson's disease, anxiety, schizophrenia or amnesia), or cell proliferative disorders (e.g. psoriasis, polycythemia vera, or cancers including adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the brain, breast, cervix or prostate).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/published_pcl_sequences](http://wipo.int/pub/published_pcl_sequences).

Sequence 1334 BP; 299 A; 381 C; 394 G; 260 T; 0 other;

Query Match 60.6%; Score 800.6; DB 25; Length 1334;
Best Local Similarity 98.3%; Pred. No. 4.8e-120;
Matches 809; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

```

OY 499 TTTGTTCCAGACATGAGATCAGGAGCTGGAGTTTGTTCATCATCATCATCTGTGGT 558
    |||||
DB 82 TCTCTCGCAAAACAGGCAATGGCGAGCTGGAGTTTGTTCATCATCATCATCTGTGGT 141
OY 559 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 618
    |||||
DB 142 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 201
OY 619 ACGGCTCTTCATATACAGCCGAGCAGAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 678
    |||||
DB 202 ACGGCTCTTCATATACAGCCGAGCAGAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 261
OY 679 AGGATGCTGTGGGCTCTTCGAGAGCAGAGTGTTCAGGCAACGAGATCCAGAGCCGAGGT 738
    |||||
DB 262 AGGATGCTGTGGGCTCTTCGAGAGCAGAGTGTTCAGGCAACGAGATCCAGAGCCGAGGT 321
OY 739 CTAGGCGCGCGCTCGCGCCACCGAGCGGCTCGCGCCGCTCGCGCCGCTCGCGCCGAGG 798
    |||||
DB 322 CTAGGCGCGCGCTCGCGCCACCGAGCGGCTCGCGCCGCTCGCGCCGCTCGCGCCGAGG 381
OY 799 CTTCACAGCGCTTCAGAGCCACCTATCTGATCTGAGAGACAGATCTGAGAGAGAGAG 858
    |||||
DB 382 CTTCACAGCGCTTCAGAGCCACCTATCTGATCTGAGAGACAGATCTGAGAGAGAGAG 441
OY 859 CATCTCGCTGTGAGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGGT 918
    |||||
DB 442 CATCTCGCTGTGAGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGGT 501
OY 919 TCGGAGACCCGAGCAGAGCTGTGAACCTGAACCGGAGAGTGTGCGCGCACCCCAAAACG 978
    |||||
DB 502 TCGGAGACCCGAGCAGAGCTGTGAACCTGAACCGGAGAGTGTGCGCGCACCCCAAAACG 561
OY 979 AACCATCTTCGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1038
    |||||
DB 562 AACCATCTTCGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 621
OY 1039 CAGTAATCTGAGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1098
    |||||
DB 622 CAGTAATCTGAGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 681
OY 1099 GCCCAGCTACAGCGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1158
    |||||
DB 682 GCCCAGCTACAGCGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 741
OY 1159 CAGTGGGCGCGCTCTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1218
    |||||
DB 742 CAGTGGGCGCGCTCTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 801
OY 1219 AGAGAGCGCAGCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1278
    |||||
DB 802 AGAGAGCGCAGCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 861
OY 1279 TCCCGAGGAGGCGGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1321
    |||||
DB 862 TCCCGAGGAGGCGGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 904
    |||||

```

RESULT 9
AA157868
ID AA157868 standard; cDNA; 1066 BP.

XX AA157868;

DE 22-OCT-2001 (first entry)

XX Human polynucleotide SEQ ID NO 71.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia; ss.

XX Homo sapiens.

XX MO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US34263.

XX 21-JAN-2000; 2000US-0488725.

XX 25-APR-2000; 2000US-0552317.

XX 09-JUL-2000; 2000US-0598042.

XX 19-JUL-2000; 2000US-0620312.

XX 03-AUG-2000; 2000US-0653450.

XX 14-SEP-2000; 2000US-0662191.

XX 19-OCT-2000; 2000US-0693036.

XX 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

XX Zhao QA, Zhou P, Goodrich R, Dirmann RT;

XX WPI; 2001-442253/47.

XX P-PSDB; AAM38712.

XX Novel nucleic acids and polypeptides, useful for treating disorders

XX such as central nervous system injuries -

XX Claim 1; SEQ ID NO 71; 10078bp; English.

The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cyostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: immune system suppression, activating/inhibiting activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.

Note: The sequence data for this patent did not form part of the printed specification.

Sequence 1066 BP; 225 A; 348 C; 325 G; 168 T; 0 other;

Query Match 59.8%; Score 790.4; DB 22; Length 1066;
Best Local Similarity 99.2%; Pred. No. 2.1e-118;
Matches 794; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

ID	ABK12142	standard; cDNA; 878 bp.	ABK12142	standard; cDNA; 878 bp.
Db	708	GGCCGTGCGCCCTTCGCCACGCGGAGACGCTCCACAGCTTCCAGCCACCATATCCGTA	649	
Oy	829	CCTGAGACAGCAGATCCAGCTGCGCCACCCACCATCTCGTGCACAGCGGGAGAGACCCCC	888	
Db	648	CCTGCAGACACAGATCCAGCTGCGCGCCACCATATTCGTCGACGCGGAGAGACCCCC	589	
Oy	889	ACCCACACAGGAGCCCTGACCTTCAGCTTCGCGGAGCCCGAGCAGCAGCTGGAACGTAA	948	
Db	588	ACCCCTACAGGAGCCCTGACCTTCAGCTTCGCGGAGCCCGAGCAGCAGCTGGAACGTAA	529	
Oy	1009	TGCCAGGCTGGGGCGCCCTTCGCGCCCGCCAGCAGTAACTCGGAGCATCAGCGCCAGTGCTA	1068	
Db	468	TGCCAGGCTGGGGCGCCCTTCGCGCCCGCCAGCAGTAACTCGGAGCATCAGCGCCAGTGCTA	409	
Oy	1069	CGGCGAGCGGGGGGCGCATGAGAGGGGGCGCGG-CCCACTTACAGAGAGGTCATCGGCCACT	1127	
Db	408	CGGCGAGCGGGGGGCGCATGAGAGGGGGCGCGG-CCCACTTACAGAGAGGTCATCGGCCACT	349	
Oy	1128	ACCCGCGGCTCCTCCTTCCAGCAGCAGCAGCAGTGGGCGCCCTCCTTGTGAGAGGGA	1187	
Db	348	ACCCGCGGCTCCTCCTTCCAGCAGCAGCAGCAGTGGGCGCCCTCCTTGTGAGAGGGA	289	
Oy	1188	CCCGGCTCCACACACACATCGCGGCCCTTAGAGAGGCGCAGCCATCTGAGCAAAAGAA	1247	
Db	288	CCCGGCTCCACACACACATCGCGGCCCTTAGAGAGGCGCAGCCATCTGAGCAAAAGAA	229	
Oy	1248	AGGATAAACAGAAAGGAGACCCCTCTTAGGGTCCCCAGGGGGGCCGGGCTGGGCTGCT	1307	
Db	228	AGGATAAACAGAAAGGAGACCCCTCTTAGGGTCCCCAGGGGGGCCGGGCTGGGCTGCT	169	
Oy	1308	AGGTGAAAAAGCAG 1321		
Db	168	AGGTGAAAAAGCAG 155		
RESULT 11				
ABK12142				
ID	ABK12142	standard; cDNA; 878 bp.	ABK12142	standard; cDNA; 878 bp.
AC	ABK12142;			
XX				
DT	05-JUN-2002 (first entry)			
XX				
DE	Mouse cDNA encoding Mechanically Induced Vascular Receptor 1, MIVR-1.			
XX				
XX	Mouse; ss; gene; MIVR-1; Mechanically Induced Vascular Receptor 1;			
XX	cytosolic; cardiant; cerebroprotective; antiarteriosclerotic;			
KW	cardiac cell; anti-apoptotic; vascular endothelial cell;			
KW	cardiac hypertrophy; myocardial infarction; stroke; arteriosclerosis;			
KW	heart failure.			
XX				
OS	Mus musculus.			
XX				
XX				
FH	Key	Location/Qualifiers		
FT	CDS	20..844		
FT		/tag= a		
FT		/product= "MIVR-1"		
PN	WO200216416-A2.			
XX				
PD	28-FEB-2002.			
XX				
PF	21-AUG-2001; 2001WO-US26089.			
XX				
PR	22-AUG-2000; 2000US-227159P.			
XX				
XX				
PA	(BGHM) BRIGHAM & WOMENS HOSPITAL INC.			
PA	(PFIZ) PFIZER INC.			
XX				

[illegible]

XX W0200216416-A2.
 XX 28-FEB-2002.
 XX 21-AUG-2001; 2001WO-US26089.
 XX 22-AUG-2000; 2000US-227159P.
 XX (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 XX (PFIZ) PFIZER INC.
 XX Lee RT, Landschulz KT, Kennedy SP, Thompson JF, Turi TG;
 XX WPI: 2002-280912/32.
 XX Novel nucleic acid molecule encoding Mechanically Induced Vascular
 XX Receptor-1 polypeptide, useful for treating cardiovascular diseases
 XX Disclosure; Page 101; 105pp; English.

The invention relates to an isolated nucleic acid molecule encoding a
 Mechanically Induced Vascular Receptor (MIVR)-1 polypeptide having
 cardiac cell anti-apoptotic activity and fragments of it provided
 they are not identical to Genbank sequences A176141.1, A1594390,
 NM_004338 and A0177461. Also included are expression vectors, host
 cells, the MIVR-1 polypeptide, MIVR-1 binding peptides, modulators of
 MIVR-1, contacting a molecule having cardiac cell anti-apoptotic activity
 with a candidate agent, where the molecule is a nucleic acid molecule
 comprising MIVR-1, IEX-1, VDP-1, BRG-2 and TIS-11d or its
 expression product, determining if the anti-apoptotic activity is
 modulated and thereby identifying a modulator. The cardiac cell anti-
 apoptotic molecules and nucleic acids of the invention are useful for
 treating, diagnosing and monitoring progression of such diseases and
 disorders as characterized by increased apoptotic cell-death of vascular
 endothelial cells e.g. cardiac hypertrophy, myocardial infarction,
 stroke, arteriosclerosis and heart failure. The present sequence
 is one of the four Genbank sequences (A176141.1) which are homologous to
 the cDNA for human MIVR-1 and which are specifically disclaimed.

Sequence 693 BP; 101 A; 205 C; 237 G; 149 T; 1 other;

Query Match 37.4%; Score 493.6; DB 24; Length 693;
 Best Local Similarity 97.4%; Pred. No. 9.3e-71;
 Matches 533; Conservative 0; Mismatches 10; Indels 4; Gaps 3;

776 CCGCCCTTCGCGCAGCGGAGCGCTTCACGCGCTTCAGCCACTATCCGACTGAG 835
 693 CCGCCCTTCGCGCAGCGGAGCGCTTCACGCGCTTCAGCCACTATCCGACTGAG 634
 836 CACGAGATCGACCTGCGCAGCCACATCTGCTGTGAGAGGGAGAGAGCCGCCACTAC 895
 633 CACGAGATCGA-CTGCGCGCCACCATCTGCTGTGAGAGGGAGAGAGCCGCCACTAC 577
 886 CAGGCGCCCTTCGACCTTCAGCTTGGGAGCCCGAGCAGCAGCTGGAAGTGAACCGGGAG 955
 576 CAGGCGCCCTTCGACCTTCAGCTTGGGAGCCCGAGCAGCAGCTGGAAGTGAACCGGGAG 517
 956 TCGGTGGCGGACCCCAAGACAGACATCTTCGACATGACCTGATGGATGTGCTCCAG 1015
 516 TCGGTGGCGGACCCCAAGACAGACATCTTCGACATGACCTGATGGATGTGCTCCAG 457
 1016 CTGGGGGCGCCCTTCGCGCAGCGGAGCTTCAGCGCCAGCTGCTACGGCAGC 1075
 456 CTGGGGGCGCCCTTCGCGCAGCGGAGCTTCAGCGCCAGCTGCTACGGCAGC 397
 1076 GCGGGGCGCATGAGAGGGGCGCGCCGACCTACACAGAGGTATGTGGCCACTACCGGGG 1135
 396 GCGGGGCGCATGAGAGGGGCGCGCCGACCTACACAGAGGTATGTGGCCACTACCGGGG 337
 1136 TCTCTCTTCACAGCAGCAGAGCAGTGGGCGCGCTTCCTTCTGGA-GGGGAGCCGGGT 1194
 336 TCTCTCTTCACAGCAGCAGAGCAGTGGGCGCGCTTCCTTCTGGA-GGGGAGCCGGGT 277

OY 1195 CCACCACACACATCGGCGCCCTAGAGAGCGCACCATCTGAGCAAAAGAGAGATATA 1254
 DB 276 CCCCCACACACATCGGCGCCCTAGAGAGCGCACCATCTGAGCAAAAGAGATATA 217
 OY 1255 ACAGAAAGAGACACCTCTCTAGAGGTCCCGAGGGGCGCGGCTGCGCTAGGTGAA 1314
 DB 216 ACAGAAAGAGACACCTCTCTAGAGGTCCCGAGGGGCGCGGCTGCGCTAGGTGAA 157
 OY 1315 AAGGCG 1321
 DB 156 AAGGCG 150

RESULT 14
 AAA75152
 ID AAA75152 standard; cDNA; 1713 BP.
 XX AAA75152;
 XX 15-JAN-2001 (first entry)

DE cDNA encoding a murine TANGO 261 polypeptide.
 XX TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267;
 XX cellular proliferation; cellular differentiation; cellular adhesion;
 XX von Willebrand factor-associated disorder; cell trafficking; cancer;
 XX hemotopoietic associated disease; atelectasis; pulmonary congestion;
 XX oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
 XX intestinal disorder; spleen associated disease; renal disorder;
 XX cardiovascular disorder; ischemic heart disease; hydrocephalus;
 XX brain herniation; iatrogenic disease; inflammation; meningitis;
 XX Alzheimer's disease; cerebral toxoplasmosis; Parkinson's disease;
 XX multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.

Mus sp.
 Key Location/Qualifiers
 CDS 2..655
 FT /tag= a
 FT /product= "TANGO 261"

W0200052022-A1.
 08-SEP-2000.
 01-MAR-2000; 2000WO-US05226.
 01-MAR-1999; 99US-0122458.

(MILL-) MILLENNIUM PHARM INC.
 Barnes TM, Holtzman DA, Sharp JD, Fraser CC;
 WPI: 2000-579269/54.
 P-PSDB; AAB18450.

Novel human and murine secreted proteins designated TANGO 216, 261,
 262, 266 and 267 useful as modulating agents of cellular processes,
 e.g. for treating cancer -
 Claim 2; Fig 6A-B; 175pp; English.

The present sequence encodes a murine TANGO 261 polypeptide. The
 specification also describes TANGO 266, TANGO 216, TANGO 262, and
 TANGO 267. The TANGO polypeptides can be used to modulate cellular
 proliferation, modulate cellular differentiation and/or modulate
 cellular adhesion. The proteins can be used to treat any von Willebrand
 factor-associated disorder, regulate extracellular matrix structuring,
 cellular adhesion, and cell trafficking and/or migration, modulate
 cellular interactions, modulate cell adhesion in proliferative
 disorders, such as cancer, modulate the proliferation, differentiation,
 and/or function of cells that appear in the bone marrow, and leukocytes,

CC treat bone marrow, blood and hematopoietic associated diseases and
 CC disorders, atelectasis, pulmonary congestion or oedema, emphysema,
 CC chronic bronchitis, bronchial asthma and bronchiectasis, intestinal
 CC disorders, spleen associated diseases, modulate renal disorders, treat
 CC cardiovascular disorders such as ischemic heart disease, modulate the
 CC proliferation, differentiation, and/or function of bone and cartilage
 CC cells and to treat bone and/or cartilage associated diseases or
 CC disorder. They may also be used to treat disorders associated with the
 CC ovaries, cerebral oedema, hydrocephalus, brain herniations, iatrogenic
 CC disease, inflammations, bacterial and viral meningitis, Alzheimer's
 CC disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis,
 CC brain cancers, hydrocephalus and encephalitis, and treat hepatic
 CC disorders.

XX
 SQ Sequence 1713 BP; 506 A; 438 C; 400 G; 369 T; 0 other;

Query Match 35.3%; Score 466.2; DB 21; Length 1713;
 Best Local Similarity 83.9%; Pred. No. 2.2e-66;
 Matches 573; Conservative 0; Mismatches 83; Indels 27; Gaps 3;

595 GCTGAGCACTACAGCTGTCTGACAGGCTCTCATCAGCCGGCAGACAGCCAGGGGGGAG 654
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 1 GCTGAGCACTACAGCTGTCTGACAGCCGGCTCTCTCATCAGCCGGCAGACAGCCAGGGGAG 60
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 655 GAGAGAGATGCCCTGTCTCAGAGAGATGCTGTGGCCCTCGAGAGCAGATGTCAG 714
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 61 GAGAGAGATGAGATGCTCTCGAGAGATGCTGTGGCCCTCGAGAGATGTCAGGTCAG 120
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 715 CAACGAAATCCAGAGCCGAGTCTACAGCCCGCTCGGCGCCAGCCAGCCCTGGCGCT 774
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 121 ---TGAATGCTCCGAGCCAGAGTCTATGCTCCGCGCCGCGCCAGTACGACTGCTGT 177
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 775 GCGGCGCTTCGCGCCAGCGGAGGCTTCCACGCTTCAGCCGACCTATCCGTAAGTCA 834
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 178 GCGGCGCTTCATCAGAGG-----AGCCATTCAGACCCAGCTATCCGTAAGTCA 228
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 835 GCAAGAGATGAGCTGCGCCAGCCAGCTATGCTGTGACAGCGGAGAGAGCCCGACCTA 894
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 229 GCACGAAATGCTGCTGACAGCCAGCTATGCTGTGATGAGGAGAGAGCCCGACCTA 288
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 895 CCAAGGCGCTGACCTGACCTGAGTGGGAGCCGAGCAGCAGCTGGAAGTGAACGCGGA 954
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 289 CCAAGGCGCTGACCTGACCTGAGTGGGAGCCGAGCAGCAGCTGGAAGTGAACGCGGA 348
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 955 GTCGTGCGCGCAACCCCAAGAAACATCTTGCAGATGACCTGATGATAGTGCAG 1014
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 349 ATCTGTGCGCGCAACCCCTTAACCGAGCATCTTGCAGATGACCTTATAGACAGCAT 408
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1015 GCTGGGCGGCGCTGCG 1074
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 409 GCTGGGCGGCGCTGCTGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 468
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 1075 CCGCGGCG 1134
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 469 CCGTGGCG 528
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 1135 GTCCTCTTCCAGCAGCAGCAGCAGCAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCT 1194
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 529 CTCCTCTTCCAGCAGCAGCAGCAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 588
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1195 CCAACGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1254
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 589 CATTCTACTGCGACATGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 633
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1255 ACAGAAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1277
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 634 ACAGAAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 656
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AC AAA75166;
 XX
 DT 15-JAN-2001 (first entry)

XX cDNA clone encoding a murine TANGO 261 polypeptide.

XX
 DE TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267;
 XX cellular proliferation; cellular differentiation; cell trafficking; cancer;
 KW von Willebrand factor-associated disorder; cell trafficking; cancer;
 KW hematopoietic associated diseases; atelectasis; pulmonary congestion;
 KW oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
 KW intestinal disorder; spleen associated disease; renal disorder;
 KW cardiovascular disorder; ischemic heart disease; hydrocephalus;
 KW brain herniation; iatrogenic disease; inflammation; meningitis;
 KW Alzheimer's disease; cerebral toxoplasmosis; Parkinson's disease;
 KW multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.

XX
 OS Mus sp.

XX
 FH key Location/Qualifiers
 FT CDS 2..655
 FT /tag- a "TANGO 261"
 FT /product-

XX
 PN WO200052022-A1.

XX
 PD 08-SEP-2000.

XX
 PF 01-MAR-2000; 2000WO-US05226.

XX
 PR 01-MAR-1999; 99US-0122458.

XX
 PA (MILL-) MILLENNIUM PHARM INC.

XX
 PI Barnes TM, Holtzman DA, Sharp JD, Fraser CC;

XX
 DR WPI, 2000-579269/54.

XX
 DR P-PSDB; AAB18464.

XX
 PT Novel human and murine secreted proteins designated TANGO 216, 261,
 PT 262, 266 and 267 useful as modulating agents of cellular processes,
 PT e.g. for treating cancer -

XX
 PS Disclosure; Page : 175pp; English.

XX
 AA75166-68 encode murine TANGO 261 proteins. The specification also
 CC describes TANGO 266, TANGO 216, TANGO 262, and TANGO 267. The TANGO
 CC polypeptides can be used to modulate cellular proliferation, modulate
 CC cellular differentiation and/or modulate cellular adhesion. The
 CC proteins can be used to treat any von Willebrand factor-associated
 CC disorder, regulate extracellular matrix structuring, cellular adhesion,
 CC and cell trafficking and/or migration, modulate cellular interactions,
 CC modulate cell adhesion in proliferative disorders, such as cancer,
 CC modulate the proliferation, differentiation, and/or function of cells
 CC that appear in the bone marrow, and leukocytes, treat bone marrow, blood
 CC and hematopoietic associated diseases and disorders, treat atelectasis,
 CC pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial
 CC asthma and bronchiectasis, intestinal disorders, spleen associated
 CC diseases, modulate renal disorders, treat cardiovascular disorders such
 CC as ischemic heart disease, modulate the proliferation, differentiation,
 CC and/or function of bone and cartilage cells and to treat bone and/or
 CC cartilage associated diseases or disorder. They may also be used to
 CC treat disorders associated with the ovaries, and cerebral oedema,
 CC hydrocephalus, brain herniations, iatrogenic disease, inflammations,
 CC bacterial and viral meningitis, Alzheimer's disease, cerebral
 CC toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers,
 CC hydrocephalus and encephalitis, and treat hepatic disorders.
 CC note: the present sequence does not appear in the specification; it was
 CC created using information provided.

XX
 SQ Sequence 1713 BP; 505 A; 439 C; 400 G; 369 T; 0 other;

Query Match 35.2%; Score 464.6; DB 21; Length 1713;

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2003, 17:43:55 ; Search time 3107 seconds

(without alignments)
10333.509 Million cell updates/sec

Title: US-09-934-249-1

Perfect score: 1321

Sequence: 1 cgaccgcggtctcgagcga.....ctgcgtaggtgaaagcag 1321

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 segs, 12152238056 residues 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: em_estbta:*
2: em_estbhm:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estcro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_luv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	866	65.6	1201	9	AL517150
2	859.4	65.1	1009	9	AL578575
3	766.8	58.0	967	13	BM641849
4	766	58.0	1046	12	BM922276

5	764.2	57.9	1201	9	AL543170	AL543170
6	736.4	55.7	916	13	BQ954555	BQ954555 AGENCOURT
7	735	55.6	951	9	AL558881	AL558881
8	715.4	54.2	1007	9	AL558882	AL558882
9	715	54.1	874	13	BX362396	BX362396
10	691.2	52.3	945	13	B0539219	B0539219 AGENCOURT
11	686.6	52.0	850	13	B0602918	B0602918 AGENCOURT
12	630.6	47.7	1207	11	AK008976	AK008976 Mus muscu
13	618.6	46.8	1079	11	BC023092	BC023092 Mus muscu
14	614.6	46.5	782	12	B0015170	B0015170 UI-H-ED1-
15	607.4	46.0	609	13	B0636742	B0636742 hdl3h06.y
16	605.8	45.9	915	13	BX344441	BX344441
17	592	44.8	888	13	BX362397	BX362397
18	578.4	43.8	890	13	B0690750	B0690750 AGENCOURT
19	570.4	43.2	973	13	B0169156	B0169156 AGENCOURT
20	567.4	43.0	729	13	B0575741	B0575741 UI-H-ED1-
21	564.8	42.8	730	12	BM677602	BM677602 UI-E-E01-
22	563.2	42.6	728	13	B0683523	B0683523 UI-CF-EC1
23	550	41.6	551	12	BM141979	BM141979 1f25a11.y
24	529.8	40.1	894	12	B1851941	B1851941 603379004
25	521	39.4	1068	13	B0522705	B0522705 AGENCOURT
26	501.6	38.0	588	12	BM483503	BM483503 536869 MA
27	493.6	37.4	693	9	A1761441	A1761441 w965f07.x
28	493.4	37.4	655	13	B0691705	B0691705 AGENCOURT
29	486	36.8	1400	12	BM559329	BM559329 AGENCOURT
30	480.8	36.4	964	13	B0859860	B0859860 AGENCOURT
31	478.6	36.2	1174	9	AL517151	AL517151
32	477.6	36.2	646	13	B0859841	B0859841 AGENCOURT
33	476.4	36.1	651	14	CB554226	CB554226 MMSF0052-
34	473.4	35.8	1017	13	BX400248	BX400248
35	468.8	35.5	1280	13	B0691500	B0691500 AGENCOURT
36	468	35.4	857	10	BG323347	BG323347 602421734
37	468	35.3	974	10	BB624904	BB624904
38	465.8	35.3	744	13	B0414421	B0414421 603670223
39	461	34.9	763	12	B1646175	B1646175 603276395
40	455.4	34.5	629	13	B0730650	B0730650 UI-E-C11-
41	453.4	34.3	949	13	BX365486	BX365486
42	452.2	34.2	618	14	CD367193	CD367193 UI-H-FR2-
43	448	33.9	626	12	BM974296	BM974296 UI-CF-EC1
44	444.2	33.6	990	13	B0691066	B0691066 AGENCOURT
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ALIGNMENTS

RESULT 1
AL517150/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AL517150
AL517150 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
CSDDA008YB23 3-PRIME, mRNA sequence.
AL517150
AL517150.2 GI:30492472
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jesse,J. and Polyes,D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12780643.
Contact: Genoscope
Genoscope, Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9945.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bin/cluster.cgi?seq=CSDDA008CA12NP1&cluster=9945.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :

FEATURES
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DA008CA12NP1.
location/Qualifiers

BASE COUNT	177 a	372 c	401 g	214 t	37 others
ORIGIN					

Query Match	65.6%	Score 866;	DB 9;	Length 1201;
Best Local Similarity	88.9%	Pred. No. 2.1e-142;		
Matches 926;	Conservative 23;	Mismatches 91;	Indels 2;	Gaps 2

QY	1060	CACGTGCTAACGGCAGCGGGCGGGCGCATGAGAGGGCGCCGCCCCACCTTACAGCGAGTGCAT	1119
Db	379	CACGTGCTAACGGCAGCGGGCGGGCGCATGAGAGGGCGCCGCCCCACCTTACAGCGAGTGCAT	320
QY	1120	CGGCACATACCCGGGGGCTCTCTTCACACAGCAGAGAGCAGTAGTGGGCGGCTCTCCTTGGCT	1179
Db	319	CGGCACATACCCGGGGGCTCTCTTCCTTCACACAGCAGAGCAGTAGTGGGCGGCTCTCTTGGCT	260
QY	1180	GGAGGGGAGCCGGGGTCCACACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAG	1239
Db	259	GGAGGGGAGCCGGGGTCCACACACACAGTGGCCCTTAAAGAGCGCAGCTTCTGGAG	200
QY	1240	CAAGAGAGAGGATAAACAGAAAGGACACCTCTTAGGGTCCCAAGGAGGGCGCGGGTGGG	1299
Db	199	CAAGAGAGAGGATTAACAGAAAGGACACCTCTTAGAGTCCCAAGGAGGGCGCGGGTGGG	140
QY	1300	GGCTGCGTAGGTGAAAAAGCGCAG	1321
Db	139	GGCTGCGTAGGTGAAAAAGCGCAG	118

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ACCESSION	CDNA clone CSODK001YC24 3'-PRIME, mRNA sequence.
VERSION	AL578575
KEYWORDS	EST.
SOURCE	GI:31316780
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	I.,W.B., Gruber,C., Tessee,J. and Polyes,D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished
COMMENT	On Feb 16, 2001 this sequence version replaced at:12942781.

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FEATURES
source      revenue_genoscope_sequence_id : CS0UDK001BBI21NP1.
            Location/Qualifiers
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Best Local Similarity 97.7%;  Pred. No. 3,1e-14;
Matches 882;  Conservative 9;  Mismatches 10;  Indels 2;  Gaps 2;

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Db 949 AGCTCAACTGCAAAAGCTCTTTCTTCCAGACATGAGATCACGAGCTGAGTTGTT 890
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Db 889 CAGATCATCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 830
OY 599 AGCCACTCAAAAGCTCTTCCAGACATGAGATCACGAGCTGAGTTGTT 658
Db 829 AGCCACTCAAAAGCTCTTCCAGACATGAGATCACGAGCTGAGTTGTT 770
OY 659 GAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 718
Db 769 GAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 710
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OY 1199 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1258
Db 230 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 171
OY 1259 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1318
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OY 1319 CAG 1321
Db 110 CAG 108

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ACCESSION B0641849
VERSION B0641849.1 GI:21766021
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homini; Homo.
1 (bases 1 to 967)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLT)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNLT at:
http://image.llnl.gov
Plate: LCM2493 row: g column: 18
High quality sequence stop: 571.
Location/Qualifiers
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/clone_lib="NIH_MGC_43"
/note="Organ: eye; Vector: pOTB1; Site_1: XhoI; Site_2:
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cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library. !"
BASE COUNT
194 a 334 c 296 g 143 t
ORIGIN
Query Match 58.0%; Score 766.8; DB 13; Length 967;
Best Local Similarity 99.1%; Pred. No. 5.5e-125;
Matches 771; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
OY 524 GAGCTGAGTTGTTGATCATCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 583
Db 1 GAGCTGAGTTGTTGATCATCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
OY 584 ATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 643
Db 61 ATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
OY 644 CAGGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 703
Db 121 CAGGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
OY 704 ACAGTGTGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 763
Db 181 ACAGTGTGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
OY 764 GGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 823
Db 241 GGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
OY 824 CCGTACCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 883
Db 301 CCGTACCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
OY 884 CCCCACCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 943
Db 361 CCCCACCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
OY 944 CTGAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1003
Db 421 CTGAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480

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OY 1004 GATATGCCAGGCTGGGGGCCCCCCCCCAGACAGTAACTCGGGCATGAGCCACG 1063
 DB 481 GATATGCCAGGCTGGGGGCCCCCCCCCAGACAGTAACTCGGGCATGAGCCACG 540
 OY 1064 TGCTACGGCAGCGGGGCGGATGAGGGGCGCGCCACCTACAGGAGGTCTATCGGC 1123
 DB 541 TGCTACGGCAGCGGGGCGGATGAGGGGCGCGCCACCTACAGGAGGTCTATCGGC 600
 OY 1124 CACTACCGGGGTCCTCTTCAGACACGACGAGACAGTGGGCGCCCTCTTGCTGGAG 1183
 DB 601 CACTACCGGGGTCCTCTTCAGACACGACGAGACAGTGGGCGCCCTCTTGCTGGAG 660
 OY 1184 GGGACCGGGCTCCACACACACATCGCGCCCTAGAGAGCGCATCTGGAGCAA 1243
 DB 661 GGGACCGGGCTCCACACACACATCGCGCCCTAGAGAGCGCATCTGGAGCAA 720
 OY 1244 GAGAGAGTAAACAGAAAGACACCTCTAGGGTCCCGAGGGGGCGGGCTGGGG 1301
 DB 721 GAGAGAGTAAACAGAAAGACACCTCTAGGGTCCCGAGGGGGCGGGCTGGGG 778

SUITE 4 BM922276

DEFINITION 1046 bp mRNA linear EST 12-MAR-2002
 LOCUS AGENCOURT.6707077 NIH_MGC_115 Homo sapiens cDNA IMAGE:5754437
 ACCESSION BM922276
 VERSION BM922276.1 GI:19372655
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 1046)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: gsapbs@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLNL2791 row: n column: 06
 High quality sequence stop: 671.
 Location/Qualifiers
 1. 1046

FEATURES
 source
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5754437"
 /lab_host="DH10B"
 /clone_id="NIH_MGC_115"
 /note="Organ: pooled brain, lung, testis; Vector: pcMV-SpOUT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research genetics tracking code 021. Note: this is a NIH_MGC library."

BASE COUNT 205 a 391 c 298 g 150 t 2 others
 ORIGIN

Query Match 58.0%; Score 766; DB 12; Length 1046;
 Best Local Similarity 95.8%; Pred. No. 7.6e-125;
 Matches 818; Conservative .0; Mismatches 32; Indels 4; Gaps 3;

OY 347 CCGGCGGAGGCCCCCGGGCGCCCGGAGCCCCCGGCGCCCGCGCCCGCGCGC 406
 DB 1 CCGGCGGAGGCCCCCGGGCGCCCGGAGCCCCCGGCGCCCGCGCGCGCGC 60
 OY 407 CCGTCATGACCGCTTGATGGGGGTCAACAGCACCGCGCGCGCGCGCGCGCGC 466
 DB 61 CCGTCATGACCGCTTGATGGGGGTCAACAGCACCGCGCGCGCGCGCGCGC 120
 OY 467 AATCTCTCTGACAGTGCACACTGCAAAAGCTCTTTGTCAGAGATGAGATCAGGAG 526
 DB 121 AATCTCTCTGACAGTGCACACTGCAAAAGCTCTTTGTCAGAGATGAGATCAGGAG 180
 OY 527 CTGAGATTGTTGATCATCATCATATGATGATGATGATGATGATGATGATGATGATGAT 586
 DB 181 CTGAGATTGTTGATCATCATCATATGATGATGATGATGATGATGATGATGATGATGAT 240
 OY 587 ACGTCCCTGTGAGCCACTACAAAGCTGTGCAAGGTCTTTCATACCGCGCACAGCAG 646
 DB 241 ACGTCCCTGTGAGCCACTACAAAGCTGTGCAAGGTCTTTCATACCGCGCACAGCAG 300
 OY 647 GGGCGGAGGAGAGAAATGCGCTGTCTCAGAAAGATGCTGTGCGCTTGAGAGACACA 706
 DB 301 GGGCGGAGGAGAGAAATGCGCTGTCTCAGAAAGATGCTGTGCGCTTGAGAGACACA 360
 OY 707 GTGTCAAGCAACGGAATCCAGAGCCGACAGTCTACGCCCGCGCTGCGCCACGACCGC 766
 DB 361 GTGTCAAGCAACGGAATCCAGAGCCGACAGTCTACGCCCGCGCTGCGCCACGACCGC 420
 OY 767 CTGGCGGTGCGCGCTTTCGCCCGACGCGGAGCGCTTCACCGCTTCAGCCACCTATCCG 826
 DB 421 CTGGCGGTGCGCGCTTTCGCCCGACGCGGAGCGCTTCACCGCTTCAGCCACCTATCCG 480
 OY 827 TACCTGACAGCAGATGACGACGTCGACCCACCATCTGCTGACAGAGGGAGAGAGCC 886
 DB 481 TACCTGACAGCAGATGACGACGTCGACCCACCATCTGCTGACAGAGGGAGAGAGCC 540
 OY 887 CCAACCTACAGAGGCGCCCTGACACCTTCAGAGTTCGAGACCGCGACAGCAGTGAACCTG 946
 DB 541 CCAACCTACAGAGGCGCCCTGACACCTTCAGAGTTCGAGAGCGAGAGAGTGAACCTG 600
 OY 947 AACCGGAGATGCGGTGGGCGCACCCCAACACAGAACCATCTTGACAGTACTGATGAT 1006
 DB 601 AACCGGAGATGCGGTGGGCGCACCCCAACACAGAACCATCTTGACAGTACTGATGAT 660
 OY 1007 AGTGCCAGGTGGGCGCGCCCTGCGCCCGACAGATGATCGGGCATCGAGCGATGAC 1066
 DB 661 AGTGCCAGGTGGGCGCGCCCTGCGCCCGACAGATGATCGGGCATCGAGCGATGAC 720
 OY 1067 TACGCGACGCGCGG-GCGCATGAGAGGGGCGCGCG-CGCACCTACAGCGAGTATCGGCG 1124
 DB 721 TACGCGACGCGCGGCGCGCATGAGAGGGGCGCGCGCGCACCTACAGGGAGGTATCGGCG 780
 OY 1125 ACTA--CCCGGGGTCCTCTTCAGACACGACGAGACAGTGGGCGCCCTCTTCTGGA 1182
 DB 781 ACTAACCAGGGGTCCTCTTCAGACACGACGAGACAGTGGGCGCCCTCTTCTGGA 840
 OY 1183 GGGGACCGCGCTC 1196
 DB 841 CTGGAAGGGGAAC 854

RESULT 5
 AL543170 1201 bp mRNA linear EST 31-MAY-2003
 LOCUS AL543170 Homo sapiens PLACENTA cot 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CS0D1004Y103 5-PRIME, mRNA sequence.
 AL543170
 ACCESSION AL543170.2 GI:31265017
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

Db 434 CCTGATGGATGCTGCGAGGCTGGGCGCCCTGCCCCCCACAGCACTAATCTGGGAGATCG 375
 QY 1057 CGCCACGTGCTACGGCAGCGGCGGCATGAGAGGGGCGCGCCACCTACAGCGAGGT 1116
 Db 374 CGCCACGTGCTACGGCAGCGGCGGCATGAGAGGGGCGCGCCACCTACAGCGAGGT 315
 QY 1117 CATGGCCACTACCCGGGGTCTCTCTCCAGCAGCAGCAGAGAGTGGGCGCCCTCTT 1176
 Db 314 CATCGCCACTACCCGGGGTCTCTCTCCAGCAGCAGCAGAGAGTGGGCGCCCTCTT 255
 QY 1177 GCTGAGGGGAGCCGGGCTCCACACACACATCGCGCCCTAGAGAGCGGAGCCATCTG 1236
 Db 254 GCTGAGGGGAGCCGGGCTCCACACACATCGCGCCCTAGAGAGCGGAGCCATCTG 195
 QY 1237 GAGCAAGAAGAGATTAACAAGAAAGACACCCCTCTTAGAGTCCCGCAGGGGCGGAGC 1296
 Db 194 GAGCAAGAAGAGATTAACAAGAAAGACACCCCTCTTAGAGTCCCGCAGGGGCGGAGC 135
 QY 1297 TGGGGCTCGTAGTGTAAGGAGCAG 1321
 Db 134 TGGGGCTCGTAGTGTAAGGAGCAG 110

RESULT 8
 LOCUS AL558882 1007 bp mRNA linear EST 31-MAY-2003
 DEFINITION AL558882 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
 ACCESSION AL558882 Homo sapiens cDNA clone CS0DJ015YF12 5-PRIME, mRNA sequence.
 VERSION AL558882.2 GI:31283015
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 1007)
 L1.W.B., Gruber,C., Jessee,J. and Polayes,D.
 Full-length cDNA libraries and normalization
 Unpublished
 On Feb 15, 2001 this sequence version replaced gi:12903838.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 9945.r For more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DJ015DC06P1a;cluster=9945.r. Contact :
 Feng Liang Email: fliang@life.techn.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DJ015DC06Q1.

FEATURES
 Source
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 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DJ015YF12"
 /cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
 /clone_line="JURKAT"
 /clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 218 a 325 c 292 g 151 t 21 others
 ORIGIN

Query Match 54.2%; Score 715.4; DB 9; Length 1007;
 Best Local Similarity 99.1%; Pred. No. 5,8e-116;
 Matches 738; Conservative 2; Mismatches 3; Indels 2; Gaps 2;

QY 577 GGTGTGATACAGTGTGCTCTGAGCCACTACAAAGTGTGTGACGGTCTTCATCAGCG 636
 Db 62 GGATGTGATACAGTGTGCTCTGAGCCACTACAAAGTGTGTGACGGTCTTCATCAGCG 121
 QY 637 GCACAGCCAGGGGCGGAGAGAGAGATCCCTGTCTTAGAGAGATGCTGTGGCCCTC 696
 Db 122 GCACAGCCAGGGGCGGAGAGAGATCCCTGTCTTAGAGAGATGCTGTGGCCCTC 181
 QY 697 GGAGAGCAGATGTACAGGAGAGAGATCCCAAGCGGAGTCTACGGCCCGCCCTCGGC 756
 Db 182 GGAGAGCAGATGTACAGGAGAGAGATCCCAAGCGGAGTCTACGGCCCGCCCTCGGC 240
 QY 757 CACCGACCGCTGTGGCGCTGCCCTTCCGCCAGGGAGAGCCCTTCACCGCTTCAGGC 816
 Db 241 CACCGACCGCTGTGGCGCTGCCCTTCCGCCAGGGAGAGCCCTTCACCGCTTCAGGC 300
 QY 817 CACCTATCCGTACTGTGACAGCAGAGATGACCTGCCACCCATCTCGCTGTAGAGCG 876
 Db 301 CACCTATCCGTACTGTGACAGCAGAGATGACCTGCCACCCATCTCGCTGTAGAGCG 360
 QY 877 GGAGAGCCCGCCACCTACAGGGGCCCTGACACCCCTCCAGCTTCGGGAGCCCGAGAGCA 936
 Db 361 GGAGAGCCCGCCACCTACAGGGGCCCTGACACCCCTCCAGCTTCGGGAGCCCGAGAGCA 420
 QY 937 GCTGGAAGTGAACCGGGAGTCCGTGCGCGCACCCCAACAGAACCATCTTCAGACATGA 996
 Db 421 GCTGGAAGTGAACCGGGAGTCCGTGCGCGCACCCCAACAGAACCATCTTCAGACATGA 480
 QY 997 CCTGATGATAGTGTCCAGGCTGGGCGCCCTGCCCCCAGCAGTAACTCTGGGAGATCG 1056
 Db 481 CCTGATGATAGTGTCCAGGCTGGGCGCCCTGCCCCCAGCAGTAACTCTGGGAGATCG 540
 QY 1057 CGCCACGTGCTACGGCAGCGGGGGGAGTGGAGAGGGGCGCCGCCACCTACAGAGAGT 1116
 Db 541 CGCCACGTGCTACGGCAGCGGGGGGAGTGGAGAGGGGCGCCGCCACCTACAGAGAGT 600
 QY 1117 CATGGCCACTACCCGGGGTCTCTCTCCAGCAGCAGCAGAGAGTGGGCGCCCTCTT 1176
 Db 601 CATGGCCACTACCCGGGGTCTCTCTCCAGCAGCAGCAGAGAGTGGGCGCCCTCTT 660
 QY 1177 GCTGAGGGGAGCCGGGCTCCACACACATCGCGCCCTAGAGAGCGGAGCCATCTG 1236
 Db 661 GCTGAGGGGAGCCGGGCTCCACACACATCGCGCCCTAGAGAGCGGAGCCATCTG 719
 QY 1237 GAGCAAGAAGAGATTAACAAGAAAGACACCCCTCTTAGAGTCCCGCAGGGGCGGAGC 1296
 Db 720 GAGCAAGAAGAGATTAACAAGAAAGACACCCCTCTTAGAGTCCCGCAGGGGCGGAGC 779
 QY 1297 TGGGGCTCGTAGTGTAAGGAGCAG 1321
 Db 780 TGGGGCTCGTAGTGTAAGGAGCAG 804

RESULT 9
 LOCUS BX362396/c 874 bp mRNA linear EST 05-MAY-2003
 DEFINITION BX362396 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
 ACCESSION BX362396 Homo sapiens cDNA clone CS0DJ014YNI 3-PRIME, mRNA sequence.
 VERSION BX362396.1 GI:30378625
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 874)
 L1.W.B., Gruber,C., Jessee,J. and Polayes,D.
 Full-length cDNA libraries and normalization
 Unpublished
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France

[illegible]

MEDLINE PUBMED REFERENCE	TITLE	JOURNAL REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES source	BASE COUNT ORIGIN	Query Match
21085660 11217851									47.7%
5	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	Nature 420, 563-573 (2002)	6 (bases 1 to 1207)	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Canini, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hirose, T., Horii, F., Imoto, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kono, H., Kouda, M., Koyama, S., Kurahara, C., Matsuyama, T., Miyazaki, A., Nishikawa, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinaigawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toyota, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.	Submitted (10-JUL-2000) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suenho-cho, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)	Location/Qualifiers 1. 1207 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM.DB:2210418102" /db_xref="MGI:1902457" /db_xref="taxon:10090" /clone="2210418102" /sex="male" /tissue_type="stomach" /clone_id="RIKEN full-length enriched mouse cDNA library" /dev_stage="adult" 391. 1173 /note="Unnamed protein product; Ned4 WW binding protein 4 (MGI:MGI:1929600) putative" /codon_start=1 /protein_id="BAB26001.1" /db_xref="GI:12843489" /db_xref="MGI:1929600" /translation="MSPARAVTAORSLSPPSEITELFEVQIVIVVVMVMTCLLSHYLSARSFISRSQARRDDGLSSGCLMPSEVSGGKEPQVYAPPRDRLVWPFLQSRSPQITDYIQLHETALPTISLSDEEPPYQGGCTGLDRLPQDLNRSVRAPNPITPDSLDITDMETMGCPSPSSNGSISTATCYSSGGRMGPPPTYSVIGHIPLGSSQHOOSNPSLSLGGTRLRLHSHIAPLEKREKRGKHPL"	200 a 459 c 374 g 173 t 1 others	47.7%	


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Db      255 GAGAGATGAGATGCTCTCGAAGATGCTCTGGGCGCCACAGAGATGAGGTGAGG-- 312
QY      717 ACGGAATCCAGAGCCGAGGTCTACGCCCCGCTCGGCCACCGACCCCTGGCGTGC 776
Db      313 -TGGATGCGGAGCAGAGGTCTATGCCCCCTCGGCCACAGTACGCTCGCTGTC 371
QY      777 GCGCCCTGCGGAGCGGAGCGGCTTCACCGCTTCAGCCGACCTATCCGCTACCTGAC 836
Db      372 CCCCCCTTATCCAGCGG-----AGCGATTCACACCCACCTACCTACCTGACG 422
QY      837 ACGAGATGACCTGCGCACCACCATCTGCTGACAGCGGAGAGAGCCCACTTACC 896
Db      423 ACGAATGCTGCTGCGCACCACCATCTGCTGATGAGGAGAGAGCCCACTTACC 482
QY      897 AAGGCCCCCGACCCCTCGAGCTTCGAGGAGCCCGAGAGAGAGTGGAACTGAACCGGAGT 956
Db      483 AAGGCCCCCGACCCCTCGAGCTTCGAGGAGCCCGAGAGAGAGTGGAACTGAACCGGAGT 542
QY      957 CGGTGCGCGCACCCTCAACAGAACCATCTTCACAGTACCTGATGATGATGATGATG 1016
Db      543 CTGTGCGCGCACCCTCAACAGAACCATCTTCGACAGTACCTGATGATGATGATGATG 602
QY      1017 TGGGCGGCGCCCTGCCCCCAGACATCTCGGCGCATCAGCGCCACCTGCTACGCGCAG 1076
Db      603 TGGGCGGCGCCCTGCTCCCGCAGACATCTCGGCGCATCAGCGCCACCTGCTACGCGCAG 662
QY      1077 GCGGCGCGCATGAGGCGCGCGCCCGCAGCTACAGAGAGTCACTGCGCCTACCGGCGT 1136
Db      663 GTGGGCGCGCATGAGGCGCGCGCCCGCAGCTACAGAGAGTCACTGCGCCTACCGGCGT 722
QY      1137 CTTCTTCAGACACAGACAGAGAGTGGCGCGCTCTGCTGAGAGGAGACCGGCTGC 1196
Db      723 CTTCTTCAGACACAGACAGAGAGTGGCGCGCTCTGCTGAGAGGAGACCGGCTGC 782
QY      1197 ACCACACACATCGCGCGCTTGAAGAGCGCAGCCATCTGAGCAAGAGAAAGATTAAC 1256
Db      783 ATCAGTCGACATTTGCCCGCCTGGA-----GAACAAGAGAAAGAGAAAC 827
QY      1257 AGAAGGACACCTCTCTAGGCTCCCGCAGGCGGCGCG 1293
Db      828 AGAAGGACACCTCTCTAGGAGTGGGCGCGGCGGCG 864

RESULT 14
BQ015170/c 782 bp mRNA linear EST 26-MAR-2002
LOCUS      UT-H-ED1-axw-k-20-0-UT.s1 NCI_CGAP_ED1 Homo sapiens cDNA clone
DEFINITION IMAGE:5834635 3', mRNA sequence.
VERSION     BQ015170.1 GI:19740071
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
KEYWORDS    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 782)
AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgaps-femail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
            cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Seq primer: M13 FORWARD
            POLYA=yes.
FEATURES
source      location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5834635"
/lisue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_ED1"
/note="Organ: Left Public Bone; Vector: pT73-Pac
(Pharmacia) with a modified polylinker; Site:1: EcoR I;
Site:2: Not I; NCI_CGAP_ED1 is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line C5. The library was constructed according to Bonaldo
, Lennon and Soares, Genome Research, 6:791-806, 1996.
First strand cDNA synthesis was primed with an oligo-dT
primer containing a Not I site. Double stranded cDNA was
ligated to an EcoR I adaptor, digested with Not I, and
cloned directionally into pT73-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GCTCAAGGCT.
TAG LIB-UT-H-ED1
TAG_TISSUE=chondrosarcoma
TAG_SEQ=CGTCAAGCT"

BASE COUNT      109 a      223 c      271 g      176 t      3 others
ORIGIN
Query Match      46.5%; Score 614.6; DB 12; Length 782;
Best Local Similarity 98.9%; Pred. No. 2,9e-98;
Matches 617; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      698 GAGAGCAGAGTGTACAGCAAGATCCAGAGCCGAGGTACGCCCCGCTCGGCC 757
Db      782 GAGAGCAGAGTGTACAGCAAGATCCAGAGCCGAGGTACGCCCCGCTCGGCC 723
QY      758 ACCGACCGCGTGGCGCGCTGCGCGCTGCGCGAGCGGAGCGGTCCACCGCTTCAGGCC 817
Db      722 ACCGACCGCGTGGCGCGCTGCGCGCTGCGCGAGCGGAGCGGTCCACCGCTTCAGGCC 663
QY      818 ACCTATCGCTACCTGAGCAGAGATGAGTGCACCTGACCATCATCTGCTGACAGCGG 877
Db      662 ACCTATCGCTACCTGAGCAGAGATGAGTGCACCTGACCATCATCTGCTGACAGCGG 603
QY      878 GAGAGCCCCCACCCTTACAGAGGCGCCCTGACCCCTCAGCTTGGGAGCCCGAGAGCAG 937
Db      602 GAGAGCCCCCACCCTTACAGAGGCGCCCTGACCCCTCAGCTTGGGAGCCCGAGAGCAG 543
QY      938 CTGGAAGTGAACGGGAGTGGGTGCGCGACCCCAACAGAGAACATCTTCAGAGTGCAG 997
Db      542 CTGGAAGTGAACGGGAGTGGGTGCGCGACCCCAACAGAGAACATCTTCAGAGTGCAG 483
QY      998 CTGATGATAGTGCAGAGGTGGGCGGCCCTGCCCCCAGCAGTAACTGGGCGATCAGC 1057
Db      482 CTGATGATAGTGCAGAGGTGGGCGGCCCTGCCCCCAGCAGTAACTGGGCGATCAGC 423
QY      1058 GCCAGTGTCTACGCGCAGCGCGGCGCGCATGAGAGGCGCCCGCCCACTACAGCGAGTGC 1117
Db      422 GCCAGTGTCTACGCGCAGCGCGGCGCGCATGAGAGGCGCCCGCCCACTACAGCGAGTGC 363
QY      1118 ATGGGCGACACTACCGGCGGTCTCTCTTCAGACACACAGCAGAGTGGGCGGCTCTCTG 1177
Db      362 ATGGGCGACACTACCGGCGGTCTCTCTTCAGACACACAGCAGAGTGGGCGGCTCTCTG 303
QY      1178 CTGAGAGGAGACCGCGGTCTCACACACACATCGCGCCCTTACAGAGCGAGCATCTGG 1237
Db      302 CTGAGAGGAGACCGCGGTCTCACACACATCGCGCCCTTACAGAGCGAGCATCTGG 243
QY      1238 AGCAAGAGAGATTAACAGAAAGACACCCCTTATAGGCTCCAGAGGCGGCGGCT 1297
Db      242 AGCAAGAGAGATTAACAGAAAGACACCCCTTATAGGCTCCAGAGGCGGCGGCT 183
QY      1298 GGGGCTGCGTAGGTGAAGAGCAG 1321

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      Db      182 GGGGTTCGTAGTGAAGCAG 159
      RESULT 15
      B0636742
      LOCUS      B0636742      609 bp      mRNA      EST 15-JUL-2002
      DEFINITION  hd13h06.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he
      ACCESSION   B0636742
      VERSION     B0636742.1 GI:21761201
      KEYWORDS    EST.
      SOURCE      Homo sapiens (human)
      ORGANISM    Homo sapiens
                  Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
      REFERENCE   1 (bases 1 to 609)
      AUTHORS     Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behl,A., Touchman
                  ,J.W., Bouffard,G., Smith,D. and Peterson,K.
                  Expressed sequence tag analysis of human retina for the NEIRBank
                  Project: Retbindin, an abundant, novel retinal cDNA and alternative
                  splicing of other retina-preferred gene transcripts
                  Mol. Vis. 8 (4), (2002) in press
      JOURNAL     Contact: Wistow G
                  Section on Molecular Structure and Function
                  National Eye Institute
                  6/331, NIH, Bethesda, MD 20892-2740, USA
                  Tel: 301 402 3452
                  Fax: 301 496 0078
                  Email: graeme@helix.nih.gov
                  Plate: 13 row: h column: 06
                  Seq primer: M13RP1 reverse primer (ABI).
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                  /mol_type="mRNA"
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                  /tissue_type="Retina"
                  /dev_stage="Adult"
                  /lab_host="EMD1108"
                  /clone_11b="Human Retina cDNA (Un-normalized, unamplified
                  ): hd/he"
                  /note="Organ: Eye; Vector: pSPORT1; Neural retina tissue
                  was dissected from two 80 year old donors with no observed
                  eye disease. 100ug of total RNA was used for library
                  construction. A directionally cloned cDNA library in the
                  pSPORT1 vector (Life Technologies) was constructed at
                  Bioserve Biotechnology (Laurel MD) essentially following
                  the protocols of the SuperScript Plasmid System full
                  details of which are contained in the manufacturer's
                  instruction manual (http://www.lifetech.com/). First
                  strand synthesis was carried out using a Not I
                  primer-adaptor [5'-pGACTAGTCTAGATCGGAGCGGCCGCC(TT)15-3'
                  ]. EST analysis was performed on the unamplified library
                  at the NIH Intramural Sequencing Center (NISC)."
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BASE COUNT 114 a 238 c 182 g 75 t

ORIGIN

Query Match 46.0%; Score 607.4; DB 13; Length 609;
 Best Local Similarity 99.8%; Pred. No. 5.2e-97;
 Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 61 GCCCTCGAGAGACAGTGTACGCAACGGAATCCAGAGCCGACAGTCTACGCCGCC 120
OY 751 TGGGCCACCGACCGCTGCGCGCTTGGCCCAAGGGAGCGCTTCCAGCGCTT 810
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Db 121 TGGGCCACCGACCGCTGCGCGCTTGGCCCAAGGGAGCGCTTCCAGCGCTT 180
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OY 1111 CGAGGTCATCGGCACTACCCGGGTCCTCTTCAGACACACAGACAGAGTGGCGCC 1170
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(Without alignments)
5949.664 Million cell updates/sec

Title: US-09-934-249-1

Perfect score: 1321

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Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues 1139956

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	755.8	57.2	759	4	US-09-769-482-2
3	352.2	26.7	921	4	US-09-091-952A-7
4	352.2	26.7	8065	4	US-09-091-952A-6
5	284.2	21.5	867	4	US-09-091-952A-8
6	70.4	5.3	4403765	3	US-09-103-840A-2
7	68.8	5.2	4411529	3	US-09-103-840A-1
8	68	5.1	44377	2	US-08-804-227C-7
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22	63.2	4.8	2991	4	US-09-335-700-48
23	62.8	4.7	2222	4	US-09-795-927-11
24	62.2	4.7	319	3	US-09-165-264-8
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C 31	59.6	4.5	4401	4	US-09-614-034-192	Sequence 192, App
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C 33	59.2	4.5	320	3	US-09-165-264-7	Sequence 7, Appl
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C 35	59	4.5	801	2	US-08-770-379-16	Sequence 16, Appl
C 36	59	4.5	801	3	US-08-757-669A-16	Sequence 16, Appl
C 37	59	4.5	801	4	US-09-298-568-3	Sequence 3, Appl
C 38	59	4.5	801	4	US-09-230-371A-16	Sequence 16, Appl
C 39	58.4	4.4	320	3	US-09-165-264-11	Sequence 11, Appl
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C 41	58.2	4.4	43280	2	US-08-804-227C-1	Sequence 1, Appl
C 42	58	4.4	44377	2	US-08-804-227C-7	Sequence 7, Appl
C 43	58	4.4	44377	2	US-08-804-198-1	Sequence 1, Appl
C 44	57.6	4.4	318	3	US-09-165-264-12	Sequence 12, Appl
C 45	56.8	4.3	2258	4	US-09-016-434-1415	Sequence 1415, Ap

ALIGNMENTS

RESULT 1	US-09-769-482-1	Sequence 1, Application US/09769482
Patent No. 6566130		
GENERAL INFORMATION:		
APPLICANT: SRIVASTAVA, SHIV		
APPLICANT: MOULI, JUDD W.		
APPLICANT: XU, LINDA L.		
APPLICANT: SEGAWA, TAKEHIKO		
TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED		
FILE REFERENCE: P04995 0057-00000		
CURRENT APPLICATION NUMBER: US/09/769,482		
CURRENT FILING DATE: 2001-01-26		
PRIOR APPLICATION NUMBER: 60/178,772		
PRIOR FILING DATE: 2000-01-28		
PRIOR APPLICATION NUMBER: 60/179,045		
PRIOR FILING DATE: 2000-01-31		
NUMBER OF SEQ ID NOS: 67		
SOFTWARE: PatentIn Ver.2.1		
SEQ ID NO 1		
LENGTH: 1140		
TYPE: DNA		
ORGANISM: Homo sapiens		
FEATURE:		
NAME/KEY: CDS		
LOCATION: (95)..(850)		
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Db	391	GGCCACCTATCCGTACTCTGCAGCAGCAGAAATGAGACTGCGACCCACCATCTGGCTTCAGA	450
OY	874	CGGGAGAGAGCGCCCGCACCCCTACCAAGGGGCGCTGCACCCCTCAGCTTCGCGAGCCCGAGACA	933
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RESULT 2
 US-09-769-482-2
 Sequence 2, Application US/09769482
 Patent No. 6566130
 GENERAL INFORMATION:
 APPLICANT: SRIVASTAVA, SHIV
 APPLICANT: MOULI, JUDD W.
 APPLICANT: XU, LINDA L.
 APPLICANT: SEGAWA, TAKEHIKO
 TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
 TITLE OF INVENTION: POYNUCEOTIDE ARRAY
 FILE REFERENCE: 04995, 0057-00000
 CURRENT APPLICATION NUMBER: US/09/769,482
 CURRENT FILING DATE: 2001-01-26
 PRIOR APPLICATION NUMBER: 60/1178,772
 PRIOR FILING DATE: 2000-01-28
 PRIOR APPLICATION NUMBER: 60/179,045
 PRIOR FILING DATE: 2000-01-31
 NUMBER OF SEQ ID NOS: 67
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 2
 LENGTH: 759
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-769-482-2

Query Match 57.2%; Score 755.8; DB 4; Length 759;
 Best Local Similarity 99.7%; Pred. No. 2,6e-133;
 Matches 757; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 1 ATGGCGGAGCGTGGAGTTGTCACATCATCATCATCTGTGGGCGATGATGATGATGCTG 60

OY	578	GTGGTGATATACCTGCGCTGTGGAGCCACTCTCAAGCTCTTGACAGCGTCCTTTCATCAGCCG	637
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Db	181	GAGAGCACAGTTCACAGGCAAGGAATCCAGAGGCCAGTCTACGCCGCCCGCTCGGGCC	240
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Db	241	ACCGACCGCGCTGGCCGTGCCGCCCTTTCGCCACGCGGGAGCGCTTTCACCGCGCTTTCAGCCC	300
OY	818	ACCTTATCCGTACCTGCAGACAGATGCATCTGCACCCACCCATCTCGCTGTGCAGCGG	877
Db	301	ACCTTATCCGTACCTGCAGACAGATGCATCTGCACCCACCCATCTCGCTGTGCAGCGG	360
OY	878	GAGGAGCCCCCACCCTACCAAGGGCCCTGCACCCCTGCAGTTCGGGAGACCCCGGACGACG	937
Db	361	GAGGAGCCCCCACCCTACCAAGGGCCCTGCACCCCTGCAGTTCGGGAGACCCCGGACGACG	420
OY	938	CTGGAACCTGAACCCGGGAGTGGTGGCGCGCACCCGCCAAACAGAACCATCTTCGACAGTGAC	997
Db	421	CTGGAACCTGAACCCGGGAGTGGTGGCGCGCACCCGCCAAACAGAACCATCTTCGACAGTGAC	480
OY	998	CTGATGATGATAGTGGCAGCGCTGGGGGGCCCTCGCCCGCCAGAGATTAACTCGGGCAATCAG	105
Db	481	CTGATGATGATAGTGGCAGCGCTGGGGGGCCCTCGCCCGCCAGAGATTAACTCGGGCAATCAG	540
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Db	541	GCCACGTCTACGGGACGCGGGCGGCATGGAGGGGCGCGGCCCACTTACAGCGAGGTC	600
OY	1118	ATCGGCACCTACCCGGGGGTCCTCTTTCGAGCAACAGAGAGTGGGGCGGCCCTCTCTTG	117
Db	601	ATCGGCACCTACCCGGGGGTCCTCTTTCGAGCAACAGAGAGTGGGGCGGCCCTCTCTTG	660
OY	1178	CTGGAGGGGAGCCCGGCTCCACACACACATCGCGGCCCTTAGAGAGCGCAGCATCTGG	123
Db	661	CTGGAGGGGAGCCCGGCTCCACACACACATCGCGGCCCTTAGAGAGCGCAGCATCTGG	720
OY	1238	AGCAAGAAGAGATTAACAGAAAGAACCCCTCTCTAG	1276
Db	721	AGCAAGAAGAGATTAACAGAAAGAACCCCTCTCTAG	759

RESULT 3
 US-09/091-952A-7
 Sequence 7, Application US/09091952A
 Patent No. 6458532
 GENERAL INFORMATION:
 APPLICANT: Detera-Wadleigh, Sevilla D.
 Gershon, Elliot S.
 Badner, Judith A.
 Goldin, Lynn R.
 Berrettini, Wade H.
 Yoshikawa, Takeo
 Sanders, Alan R.
 Esterling, Lisa E.
 TITLE OF INVENTION: Chromosomal Markers and Diagnostic
 Tests for Manic-Depressive Illness
 NUMBER OF SEQUENCES: 197
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-OCT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1...921
OTHER INFORMATION: Clone 22 coding region
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-091-952A-7
Query Match 26.7%; Score 352.2; DB 4; Length 921;
Best Local Similarity 73.1%; Pred. No. 9,5e-58;
Matches 482; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

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986 TTGACAGTGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1042

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1043 AACCTGGGATCAGGCGCGCGCTGATGATGATGATGATGATGATGATGATGATGATG 1102
700 AACCTGGGATCAGGCGCGCGCTGATGATGATGATGATGATGATGATGATGATGATG 759
1103 AACCTGGGATCAGGCGCGCGCTGATGATGATGATGATGATGATGATGATGATGATG 1161
760 AACCTGGGATCAGGCGCGCGCTGATGATGATGATGATGATGATGATGATGATGATG 818

RESULT 4
US-09-091-952A-6
Sequence 6, Application us/09091952A
Patent No. 6458532
GENERAL INFORMATION:
APPLICANT: Detera-Wadleigh, Sevilla D.
Gershon, Elliot S.
Badner, Judith A.
Goldin, Lynn R.
Berrellini, Wade H.
Yoshikawa, Takeo
Sanders, Alan R.
Estherling, Lisa E.
TITLE OF INVENTION: Chromosomal Markers and Diagnostic Tests for Manic-Depressive Illness
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-OCT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8065 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: -
LOCATION: 1...8065
OTHER INFORMATION: Clone 22
FEATURE:
NAME/KEY: CDS
LOCATION: 116...1036
OTHER INFORMATION: Clone 22 coding region

NAME/KEY:	misc:feature
LOCATION:	452...505
OTHER INFORMATION:	alternatively spliced portion
NAME/KEY:	misc:feature
LOCATION:	5595...5685
OTHER INFORMATION:	amplified region for genotyping
SEQUENCE DESCRIPTION:	SEQ ID NO: 6
US-09-091-952A-6	
Query Match	26.7%; Score 352.2; DB 4; Length 8065;
Best Local Similarity	73.1%; Pred. No. 1.3e-57;
Matches	482; Conservative 0; Mismatches 168; Indels 9; Gaps 2;
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Db	566 ATGTGATGT 625
Db	341 ACGGTGATGT 400
Db	626 TTCATCAGCCGCGGACAGCCAGGGGGGGAGAGAGATGTGCTGTCTCCAGAAAGATGC 685
Db	401 TTCTATCAACGCCGCCGACACAGCCGGAGGGGGAGGGAGGCTGCGCCAGAGAGGGTGC 460
Db	686 CTGTGGCCCTTGGAGAGCAGAGTGTCAAGCAGGAAATCCAGAGCCGAGGTCTACGCC 745
Db	461 CTGTGGCCCTTGGAGAGCAGAGTGTCAAGCAGGAAATCCAGAGCCGAGGTCTACGCC 514
Db	746 CCGGCTGGGGCCACCGACCGGCTGGCGTGGCGCCCTTGGCGCCAGAGGGAGGCTTCCAC 805
Db	515 GCCCGCGGCTTCCAGGAGACAGGTTCACAGCGCCGCTCTTCATTCAGAGGGATCGCTCAGC 574
Db	806 CGCTTCCAGCCACCTATCCGTACTCGTACGAGACAGATGAGACTGACACCCACCATCTCG 865
Db	575 CGCTTCCAGCCACCTATCCGTACTCGTACGAGACAGATGAGACTGAGACTGAGCTTC 634
Db	866 CTGTTCAGAGGGGGAGAGAGCCCTTACAGAGGGCCCTTCAGCCCTTCAGCTTGGGAGC 925
Db	635 CTGTTCAGAGGGGGAGAGAGCCCTTACAGAGGGCCCTTCAGCCCTTCAGCTTGGGAGC 694
Db	926 CCGGAGCAGCAGCTGAGAACTGACCGGGAGTCTGGGCGCGACCCGCAAGAGAGATC 985
Db	695 CCGGAGCAGCAGCTGAGAACTGACCGGGAGTCTGGGCGCGACCCGCAAGAGATC 754
Db	986 TTGCAGAGTGAAGT 1042
Db	755 TTGCAGAGTGAAGT 814
Db	1043 AACCTGGGCAATCAGCGGACAGTGTCTAGCGGACGGGGGGGGGGGGGGGGGGGGGGGG 1102
Db	815 AACCTGGGCAATCAGCGGACAGTGTCTAGCGGACGGGGGGGGGGGGGGGGGGGGGGGG 874
Db	1103 ACCTAGACGAGATGATACGAGCTGAGTTTGTTCAGATCATCATGCTGGTGGTATG 1161
Db	875 ACATACAGCGAGT 933
RESULT 5	
US-09-091-952A-8	
Sequence 8, Application US/09091952A	
Patent No. 6458532	
GENERAL INFORMATION:	
APPLICANT:	Deterra-Wadleigh, Sevilla D.
	Gershon, Elliot S.
	Badner, Judith A.
	Goldin, Lynn R.
	Berrettini, Wade H.
	Yoshikawa, Takeo
	Sanders, Alan R.
	Esterling, Lisa E.
TITLE OF INVENTION:	Chromosomal Markers and Diagnostic

	NUMBER OF SEQUENCES:	197	Tests for Manic-Depressive Illness
	CORRESPONDENCE ADDRESS:		
	ADDRESSEE:	Townsend and Townsend and Crew LLP	
	STREET:	Two Embarcadero Center, Eighth Floor	
	CITY:	San Francisco	
	STATE:	CA	
	COUNTRY:	USA	
	ZIP:	94111-3834	
	COMPUTER READABLE FORM:		
	MEDIUM TYPE:	Diskette	
	OPERATING SYSTEM:	DOS	
	SOFTWARE:	Fasteq for Windows Version 2.0	
	CURRENT APPLICATION DATA:		
	APPLICATION NUMBER:	US/09/091,952A	
	FILING DATE:	19-Apr-1999	
	CLASSIFICATION:	<unknown>	
	PRIOR APPLICATION DATA:		
	APPLICATION NUMBER:	US 60/029,278	
	FILING DATE:	28-OCT-1996	
	APPLICATION NUMBER:	PCT/US97/19381	
	FILING DATE:	28-OCT-1997	
	ATTORNEY/AGENT INFORMATION:		
	NAME:	Smith, Timothy L.	
	REGISTRATION NUMBER:	35,367	
	REFERENCE/DOCKET NUMBER:	015280-297100US	
	TELECOMMUNICATION INFORMATION:		
	TELEPHONE:	(415) 576-0200	
	TELEFAX:	(415) 576-0300	
	TEXT:	<unknown>	
	INFORMATION FOR SEQ ID NO: 8:		
	SEQUENCE CHARACTERISTICS:		
	LENGTH:	867 base pairs	
	TYPE:	nucleic acid	
	STRANDEDNESS:	single	
	TOPOLOGY:	linear	
	MOLECULE TYPE:	cdna	
	FEATURE:		
	NAME/KEY:	CDS	
	LOCATION:	1...867	
	OTHER INFORMATION:	Clone 22 Isoform 2 alternatively spliced coding region	
	SEQUENCE DESCRIPTION:	SEQ ID NO: 8:	
	US-09-091-952A-8		
	Query Match	21.5%; Score 284.2; DB 4; Length 867;	
	Best Local Similarity	68.7%; Pred. No. 5e-45;	
	Matches	453; Conservative 0; Mismatches 143; Indels 63; Gaps 2	
QY	506 CAGAGCATGGAGATCAGGACGTGGAGTTTGTTCAGATCATCATCGTGSTGATG	565	
DB	166 CCGGGGCATCTTCAACTCGAGCTGGAGTGCACCACAAATCATCATCATCGTGSTGATC	225	
QY	566 ATGTGTGATGGGTGGTATCACGTCGCTGCTGAGACCACTAACCTGTCACAGGTC	625	
DB	226 ACGGTGATGGGTGGTATCATCGTCTGCTGCTGAACCACTAAGTCTCCACGGGTC	285	
QY	626 TTTCATCAGCGCGGACAGGAGGGGCGGAGAGAGAAGATGCCCTTCAGAAAGATGC	685	
DB	286 TTCATCAACCGCCGGAACAGAGCGCGGAGGCGGAGACGGGCT-----	329	
QY	686 CTGTGGCCCTGGAGAGACAGTGTTCAGGCAAGGATCCAGAGCCCGCAGGTCTACGCC	745	
DB	330 -----GCCGACGATCATGAT	345	
QY	746 CCAGCTCGGCCACCGACCGCTGGCGCTGCGCCCTTCGCCACGGAGGAGCTTCAC	805	
DB	346 GCCCGGGGTTCAGAGGAGTTCACAGCGCGCTTCATTCACAGAGGATCGCTTCAC	405	
QY	806 CGCTTCACGCCACCTATCGTACCTGACGACAGATGCACTTCACACCAACCATCTCG	865	
	406 CGCTTCACGCCACCTATCGTACCTGAGAGAGAGATGATTCCTCCACCATCTTC	465	

QY 866 CTGTACAGAGGGGAGAGCCCTACAGAGGGCCCTTCAGCTTCAGCTTCGGAGC 925
DB 466 CTGTCCGACGGTGAAGAGCCACTCTTACAGAGGGGCTTCAGCTTCAGCTTCGGAGC 525
QY 926 CCGGACGACGAGCTGAGTGAACCGGAGTGTGGCGGACCCCAACAGAACATC 985
DB 526 CCGTGAACGACAGATGAATCAACCGAGAGTCCGAGAGGGCCCAACAGAACATC 585
QY 986 TTGACAGTGAAGTGAATGATGACAGG--CTGGGCGGCGCTTCGCCCCCAGCAGT 1042
DB 586 TTGACAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 645
QY 1043 AACTGCGGATCAGCGCCACGTCATGACGAGCGGCGGCGGCGGAGGAGGCGCGCC 1102
DB 646 AACTGCGGATCAGCGCCACGTCATGACGAGCGGAGGAGGAGGAGGAGGAGGAGG 705
QY 1103 AACTGCGGAGTGTATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1161
DB 706 AACTGCGGAGTGTATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 764

RESULT 6

US-09-103-840A-2
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT FILING DATE: 1998-06-24
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2

Query Match 5.3%; Score 70.4; DB 3; Length 4403765;

Best Local Similarity 50.0%; Pred. No. 0.00016;
Matches 230; Conservative 0; Mismatches 226; Indels 4; Gaps 2;

QY 2 GACGCGGCTGCGGAGCGAACCAGATCTCTGACCTGATGATGAGAGAGAGGCGGC 61
DB 3936335 GCGGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3936394
QY 62 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 121
DB 3936395 ATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3936454
QY 122 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
DB 3936455 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3936514
QY 181 -ACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 239
DB 3936515 CAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3936574
QY 240 CTGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 299
DB 3936575 AACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3936634
QY 300 CTTCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 359

DB 3936635 GCGTCTCTAGCTACCAACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3936692
QY 360 CCG 419
DB 3936693 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3936752
QY 420 GCTTGTATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 459
DB 3936753 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3936792

RESULT 7

US-09-103-840A-1
Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT FILING DATE: 1998-06-24
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 5.2%; Score 68.8; DB 3; Length 4411529;
Best Local Similarity 49.8%; Pred. No. 0.00033;
Matches 229; Conservative 0; Mismatches 227; Indels 4; Gaps 2;

QY 2 GACGCGGCTGCGGAGCGAACCAGATCTCTGACCTGATGATGAGAGAGAGGCGGC 61
DB 3942788 GCGGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3942847
QY 62 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 121
DB 3942848 ATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3942907
QY 122 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
DB 3942908 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3942967
QY 181 -ACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 239
DB 3942968 CAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3943027
QY 240 CTGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 299
DB 3943028 AACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3943087
QY 300 CTTCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 359
DB 3943088 GCGTCTCTAGCTACCAACGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3943145
QY 360 CCGG 419
DB 3943146 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3943205
QY 420 GCTTGTATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 459
DB 3943206 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3943245

RESULT 8

US-08-804-227C-7/c
; Sequence 7, Application US/08804227C
; Patent No. 5876991
; GENERAL INFORMATION:
; APPLICANT: Dehoff, Bradley S.
; APPLICANT: Kuhstoss, Stuart A.
; APPLICANT: Rostock, Paul R., Jr.
; APPLICANT: Sutton, Kimberly L.
; TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THOMAS G. PLANT 1501
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII(DOS) Text only
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804.227C
; FILING DATE: February 21, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Plant, Thomas, G.
; REGISTRATION NUMBER: 35, 784
; REFERENCE/DOCKET NUMBER: X-8231
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-2459
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4437 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 350..14002
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 14046..20036
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 20110..31284
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31329..36071
; NAME/KEY: CDS
; LOCATION: 36155..41830
US-08-804-227C-7

Query Match 5.18; Score 68; DB 2; Length 44377;
Best Local Similarity 49.2%; Pred. No. 0.00025;
Matches 234; Conservative 0; Mismatches 240; Indels 2; Gaps 2;

QY 5 CGCGGTCTCGAGCGAAACCGGATCTCCCTTGGAATTGAGAGAGAGAGCGCGCGC 64
DB 19499 CTGGGGTGGCGGAACGTCCCGGAGCGCGCGGCGCACCGTCCCGGCGCGTCCGCGGCGC 19440
QY 65 GCGCGGCGCGCGCGCGCTGCGGAAAGCTAGCGGAGAGAGCGCTCACCGCGCGC 124
DB 19439 GGGGGGCGAGGCGCGACGCGCTCTCGTCCCGGTGCGCGCGCGCGCGCGGTGCT 19380
QY 125 GCAGCGCGCGCGCGCGCTGCGACGCCATTTTCGAGCGCCCGCGCGCGCTGCGAGCG 184
DB 19379 GCGGGGCTGCG 19320
QY 185 CCCCGGGGCTGCGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 244

DB 19319 GCGCGGCGCGCGCGCGAGTGAAGCCGACGAGGAGCGGCGCGCTCGGCGCGCGGT-CAGCG 19261
QY 245 CCGCGCGCGCGCGCGCGGAGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 304
DB 19260 CCGGCTGAGCGAGTGCAGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 19201
QY 305 CCG 364
DB 19200 CCG 19141
QY 365 GCG 424
DB 19140 AGCGAGCGAGCG 19082
QY 425 ATGGGGTGCACACAGCG 19082
DB 19081 AAGCGGTGGCGCGCGCGGTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 19026

RESULT 9
US-08-804-198-1/c
; Sequence 1, Application US/08804198
; Patent No. 5945320
; GENERAL INFORMATION:
; APPLICANT: Burgelt, Stanley G.
; APPLICANT: Kuhstoss, Stuart A.
; APPLICANT: Rao, Nagendra R.
; APPLICANT: Richardson, Mark A.
; APPLICANT: Rostock, Paul R., Jr.
; TITLE OF INVENTION: PLATENOIDE SYNTHASE GENE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PAUL R. CANTRELL 1138
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804.198
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CANTRELL, PAUL R.
; REGISTRATION NUMBER: 36, 470
; REFERENCE/DOCKET NUMBER: 9113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-3885
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4437 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 350..14002
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 14046..20036
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 20110..31284
; NAME/KEY: CDS
; LOCATION: 31329..36071


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1      FILING DATE: 02-JUNE-1995
2      CLASSIFICATION: 435
3      PRIOR APPLICATION DATA:
4      APPLICATION NUMBER: US 08/065,146
5      FILING DATE: 03-MAY-1993
6      CLASSIFICATION: 435
7      ATTORNEY/AGENT INFORMATION:
8      NAME: Leary Ph.D., Kathryn R.
9      REGISTRATION NUMBER: 36,317
10     REFERENCE/DOCKET NUMBER: DFIG-0029
11     TELECOMMUNICATION INFORMATION:
12     TELEPHONE: (215) 568-3100
13     TELEFAX: (215) 568-3439
14     INFORMATION FOR SEQ ID NO: 11:
15     SEQUENCE CHARACTERISTICS:
16     LENGTH: 12001 base pairs
17     TYPE: nucleic acid
18     STRANDEDNESS: double
19     TOPOLOGY: linear
20     MOLECULE TYPE: DNA (genomic)
21     HYPOTHEetical: NO
22     ANTI-SENSE: NO
23     ORIGINAL SOURCE:
24     ORGANISM: Herpes simplex virus
25     STRAIN: Herpes Simplex Virus Type 1
26     US-08-458-11

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LENGTH: 152331
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(152331)
OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

Query Match 5.0%; Score 66; DB 3; Length 152331;
Best Local Similarity 49.1%; Pred. No. 0.0007;
Matches 189; Conservative 0; Mismatches 191; Indels 5; Gaps 1;

QY 75 GCGGAGGCGCTCGGCTGGGGAAGCTAGCGGCGAGAGCTCAGCCCGCGGCGAGCGGCG 134
DB 21828 GGGGTGTGACGTGGGTGGGTGTGTGGGTGGNACNNNNNNNNNNNNNNNNNNNNNN 21887
QY 135 CCGCGCTGCGAGGCGCATTTCCGAGCGCACCGCGGCGACTGCGAGCGCCCGCGGCGT 194
21888 CCG 21942
195 GCGGAGGCGAGCGCGGCGGCGCGAGCGAGCGGCGTCCGCGACTGAGCGCGCGCG 254
DB 21943 CCG 22002
QY 255 CCGCGGGAAGTGGGCGGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 314
DB 22003 CCG 22062
QY 315 GCGTCTGTCATGCGGCGCGCGAGCTCCGCGCGCGCGGAGCGCGCGCGCGCGCGCG 374
DB 22063 CCG 22122
QY 375 GAGCG 434
DB 22123 CCG 22182
QY 435 ACAGACG 459
DB 22183 CCG 22207

Search completed: August 27, 2003, 20:11:11
Job time : 133 secs

17	182	13.8	467	11	US-09-918-995-2074	Sequence 2074, Ap
18	78	5.9	4020	11	US-09-966-679-5	Sequence 5, Appl1
19	75.4	5.7	2561	10	US-09-976-740-48	Sequence 48, Appl1
20	75.4	5.7	2561	13	US-10-023-529-48	Sequence 48, Appl1
21	75.4	5.7	2561	13	US-10-023-529-48	Sequence 48, Appl1
22	72.2	5.5	2307	11	US-09-893-519A-87	Sequence 87, Appl1
23	72.2	5.5	2561	10	US-09-976-740-48	Sequence 48, Appl1
24	72.2	5.5	2561	13	US-10-023-529-48	Sequence 48, Appl1
25	72.2	5.5	2561	13	US-10-023-529-48	Sequence 48, Appl1
26	69.6	5.3	1746	14	US-10-156-761-4388	Sequence 4388, Ap
27	69.6	5.3	9025608	14	US-10-156-761-1	Sequence 1, Appl1
28	69.2	5.2	1117	12	US-10-017-161-1403	Sequence 1403, Ap
29	68.4	5.2	1316	14	US-10-097-340-11	Sequence 11, Appl1
30	68.4	5.2	1316	14	US-10-171-311-15	Sequence 15, Appl1
31	68	5.1	8841	10	US-09-954-531-1351	Sequence 1351, Ap
32	67.8	5.1	1260	14	US-10-156-761-3424	Sequence 3424, Ap
33	67.6	5.1	3133	12	US-10-017-161-1483	Sequence 1483, Ap
34	67.6	5.1	4257	10	US-09-825-288A-1	Sequence 1, Appl1
35	67.4	5.1	3163	12	US-10-017-161-1857	Sequence 1857, Ap
36	67.4	5.1	43058	10	US-09-954-456-252	Sequence 252, Ap
37	67.4	5.1	43058	10	US-09-954-456-529	Sequence 529, Ap
38	67.4	5.1	43058	10	US-09-880-107-39350	Sequence 39350, Ap
39	67	5.1	2028	14	US-10-156-761-3359	Sequence 3359, Ap
40	67	5.1	2826	14	US-10-025-567A-43	Sequence 43, Appl1
41	67	5.1	12733	14	US-10-032-393-47	Sequence 47, Appl1
42	67	5.1	12739	14	US-10-032-393-8	Sequence 8, Appl1
43	67	5.1	9025608	14	US-10-156-761-1	Sequence 1, Appl1
44	66.6	5.0	1614	10	US-09-976-740-45	Sequence 45, Appl1
45	66.6	5.0	1614	13	US-10-023-529-45	Sequence 45, Appl1

RESULT 1

```

US-09-934-249-1
Sequence 1, Application US/09934249
Patent No. US20020115081A1
GENERAL INFORMATION:
APPLICANT: Lee, Richard T.
APPLICANT: Landschulz, Katherine T.
APPLICANT: Turti, Thomas G.
APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
FILE REFERENCE: CARDIOVASCULAR CONDITIONS
FILE REFERENCE: P0738/7001/ERP/KA
CURRENT APPLICATION NUMBER: US/09/934,249
CURRENT FILING DATE: 2001-08-21
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1321
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (413)...(1273)
US-09-934-249-1

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Query Match	100.0%;	Score 1321;	DB 10;	Length 1321;
Best Local Similarity	100.0%;	Pred. No. 9.2e-282;		
Matches 1321; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

[illegible]

0Y	573	TGGTGTGGTATATACAGTGGCTGCTGAGGCCACTACAGCTTCTGACGGTCTTATCA	632
Db	481	TGGTGTGTATATACGTGCTGCTGAGCCACTACAGCTTCTGACGGTCTTATCA	540
0Y	633	GCCGGACAGCCAGGGGGGAGAGAGAAGATGGCTGCTCTCAAGGATGCTGTGGC	692
Db	541	GCCGGACAGCCAGGGGGGAGAGAGAAGATGGCTGCTCTCAAGGATGCTGTGGC	600
0Y	693	CCTGGAGAGACAGTGTTCAGGCAACGGAATCCAGAGCCGAGCTACGCCGCCCTC	752
Db	601	CCTGGAGAGACAGTGTTCAGGCAACGGAATCCAGAGCCGAGCTACGCCGCCCTC	660
0Y	753	GGCCACACGAGCCGCTGGCCGCTGGCCGCTTCCGCCACAGCGGAGCGCTTCCACCGCTTC	812
Db	661	GGCCACACGAGCCGCTGGCCGCTGGCCGCTTCCGCCACAGCGGAGCGCTTCCACCGCTTC	720
0Y	813	AGCCACACTATCCGATCTGACGACAGAGATCGACCTGCCACCCACCATCTCGCTGTCAG	872
Db	721	AGCCACACTATCCGATCTGACGACAGAGATCGACCTGCCACCCACCATCTCGCTGTCAG	780
0Y	873	ACGGGAGAGAGCCGCCACCTTACAGAGGGGCCCTTGCACTTCACGTTCCGGAGCCCGAGC	932
Db	781	ACGGGAGAGAGCCGCCACCTTACAGAGGGGCCCTTGCACTTCACGTTCCGGAGCCCGAGC	840
0Y	933	AGCAGCTGGAAGTGAACCGGGAGATGTCGGCGCGGACCCCGCAAGAAAGAACATCTTCGACA	992
Db	841	AGCAGCTGGAAGTGAACCGGGAGATGTCGGCGCGGACCCCGCAAGAAAGAACATCTTCGACA	900
0Y	993	GTCAGCTGATGATAGTGTCCACAGGCTGGGCGGCCCTTGCCCCCGACAGATGTAATCGGGCA	1052
Db	901	GTCAGCTGATGATAGTGTCCACAGGCTGGGCGGCCCTTGCCCCCGACAGATGTAATCGGGCA	960
0Y	1053	TCAGGCGCAGTGTCTACGGCAGCGGGGGGCGCATGTGAGAGGGGCGCGGCCACCTACAGCG	1112
Db	961	TCAGGCGCAGTGTCTACGGCAGCGGGGGGCGCATGTGAGAGGGGCGCGGCCACCTACAGCG	1020
0Y	1113	AGGTCATGGGGCAGTACCCGGGGGTCCTCTCCAGCANACAGACAGAGTGGGGCGCCCT	1172
Db	1021	AGGTCATGGGGCAGTACCCGGGGGTCCTCTCCAGCANACAGACAGAGTGGGGCGCCCT	1080
0Y	1173	CCTTGCTGAGAGGGGACCCGGCTCCACACACACACATGCGCCCTTAGAGAGCGACGCA	1232
Db	1081	CCTTGCTGAGAGGGGACCCGGCTCCACACACACACATGCGCCCTTAGAGAGCGCGACGA	1140
0Y	1233	TCTGGAGCAAAAGAGAGATTAACAGAAAGACACCTCTTAGGGTCCCGAGGGGGCC	1292
Db	1141	TCTGGAGCAAAAGAGAGATTAACAGAAAGACACCTCTTAGGGTCCCGAGGGGGCC	1200
0Y	1293	GGGCTGGGGCTGCGTAGGTGAAGAAAGGCG	1321
Db	1201	GGGCTGGGGCTGCGTAGGTGAAGAAAGGCG	1229
RESULT 3			
US-09-934-249-3			
: Sequence 3, Application US/09934249			
: Patent No. US20020115081A1			
: GENERAL INFORMATION:			
: APPLICANT: Lee, Richard T.			
: APPLICANT: Landschulz, Katherine T.			
: APPLICANT: Turi, Thomas G.			
: APPLICANT: Thompson, John F.			
: APPLICANT: Kennedy, Scott P.			
: TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF			
: TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS			
: FILE REFERENCE: P0738/7001/ERP/TA			
: CURRENT APPLICATION NUMBER: US/09/934,249			
: CURRENT FILING DATE: 2001-08-21			
: PRIOR APPLICATION NUMBER: US 60/227,159			
: PRIOR FILING DATE: 2000-08-22			
: NUMBER OF SEQ ID NOS: 17			
: SOFTWARE: FastSeq for Windows Version 3.0			

```

; SEQ_ID NO: 3
; LENGTH: 861
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(861)
US-09-934-249-3

Query Match      65.2%; Score 861; DB 10; Length 861;
Best Local Similarity 100.0%; Pred. No. 1,6e-180;
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      413  ATGCACCGCTGATGGGGGTCAACAGACACCCCGCCCGCCGGCCGGGACGCCAATGTC 472
         |||||||
Db       1  ATGCACCGCTGATGGGGGTCAACAGACACCGCCCGCCCGCCGGGACGCCAATGTC 60

OY      473  TCCTGCAGCTGCACACTGCMAAGCGCTCTTTGTTCCAGAGCATGAGATCACGAGCTGAG 532
         |||||||
Db       61  TCCTGCAGCTGCACACTGCMAAGCGCTCTTTGTTCCAGAGCATGAGATCACGAGCTGAG 120

OY      533  TTTGTTCGATCATCATCATATGCTGGTGTATGATGATGATGGTGGTGGTATCACTGC 592
         |||||||
Db       121  TTTGTTCGATCATCATCATATGCTGGTGTGTGATGATGATGGTGGTGGTATCACTGC 180

OY      593  CTGCTGAGCCCACTACAAAGCTGTCTGCAAGCGATCCATCACCGGCAAGCAGAGGGCGG 652
         |||||||
Db       181  CTGCTGAGCCCACTACAAAGCTGTCTGCAAGCGATCCATCACCGGCAAGCAGAGGGCGG 240

OY      653  AGAGAGAAGATGCCCTGTCTCAGAAAGATGCTGTGGCCCTCGGCGGAGACACAGTGTCA 712
         |||||||
Db       241  AGGAGAGAAGATGCCCTGTCTCAGAAAGATGCTGTGGCCCTCGGCGGAGACAGTGTCA 300

OY      713  GGCAACGGAATCCCAAGACCGGAGCTGTACGCCCGCCCTCGGCGCCACCGACCGCTGGCC 772
         |||||||
Db       301  GGCAACGGAATCCCAAGACCGGAGCTGTACGCCCGCCCTCGGCGCCACCGACCGCTGGCC 360

OY      773  GTGCCGCCCTTGGCCACAGCGGAGCGCTTCACCGCTTCACGCCACCTATCCGTACTGT 832
         |||||||
Db       361  GTGCCGCCCTTGGCCACAGCGGAGCGCTTCACCGCTTCACGCCACCTATCCGTACTGT 420

OY      833  CAGCAGCAGATCGACCTGCCACCAACCATCTTCGCTGTACAGCGGGAGAGACCCCAACC 892
         |||||||
Db       421  CAGCAGCAGATCGACCTGCCACCAACCATCTTCGCTGTACAGCGGGAGAGACCCCAACC 480

OY      893  TACCAAGGCGCCCTGCACCCCTCAGCTTCAGGATTCGGGAGCCCGGAGCAGCTGGAACCTAACC 952
         |||||||
Db       481  TACCAAGGCGCCCTGCACCCCTCAGCTTCAGGATTCGGGAGCCCGGAGCAGCTGGAACCTAACC 540

OY      953  GAGTCGGTGGCGGCACCCCAAGCAAGAACATCTTTCGACAGTGAACCTGATGATAGTCC 1012
         |||||||
Db       541  GAGTCGGTGGCGGCACCCCAAGCAAGAACATCTTTCGACAGTGAACCTGATGATAGTCC 600

OY      1013  AGGCTGGGGCGGGCCCTGTGCCCGCCCAAGCATTCGAGATCGGGCATCACGGCAGCTGTACGGC 1072
         |||||||
Db       601  AGGCTGGGGCGGGCCCTGTGCCCGCCCAAGCATTCGAGATCGGGCATCACGGCAGCTGTACGGC 660

OY      1073  AGCGCGGGGCGCATGAGAGGGGCGCGCGCCCACTACAGCGAGGTATTCATGGCCACTACCG 1132
         |||||||
Db       661  AGCGCGGGGCGCATGAGAGGGGCGCGCGCCCACTACAGCGAGGTATTCATGGCCACTACCG 720

OY      1133  GGGTCTCTCTTCACAGACACAGCAGAGCAGTGGGCGCCCTCTCTTGTCTGAGAGGACCCGG 1192
         |||||||
Db       721  GGGTCTCTCTTCACAGACACAGCAGAGCAGTGGGCGCCCTCTCTTGTGAGAGGACCCGG 780

OY      1193  CTCACACACACACATGCGCGCCCTTAGAGAGCGCAGGCAATCTGAGAGAAAGAGAGAT 1252
         |||||||
Db       781  CTCACACACACACATGCGCGCCCTTAGAGAGCGCAGGCAATCTGAGAGAAAGAGAGAT 840

OY      1253  AAACGAAAGAGACACCTCTC 1273
         |||||||
Db       841  AAACGAAAGAGACACCTCTC 861

```

RESULT 4
 US-09-796-753-55
 Sequence 55, Application US/09796753
 Publication No. US20030027998A1
 GENERAL INFORMATION:
 APPLICANT: McCarthy, Sean A.
 TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
 FILE REFERENCE: 7853-227-999
 CURRENT APPLICATION NUMBER: US/09/796,753
 CURRENT FILING DATE: 2001-03-01
 PRIOR APPLICATION NUMBER: 09/183,175
 PRIOR FILING DATE: 1998-10-30
 PRIOR APPLICATION NUMBER: 09/223,094
 PRIOR FILING DATE: 1998-12-30
 PRIOR APPLICATION NUMBER: 09/223,546
 PRIOR FILING DATE: 1998-12-30
 PRIOR APPLICATION NUMBER: 09/224,246
 PRIOR FILING DATE: 1998-12-30
 PRIOR APPLICATION NUMBER: 09/259,388
 PRIOR FILING DATE: 1999-02-26
 PRIOR APPLICATION NUMBER: 60/122,458
 PRIOR FILING DATE: 1999-03-01
 PRIOR APPLICATION NUMBER: 09/312,359
 PRIOR FILING DATE: 1999-05-14
 PRIOR APPLICATION NUMBER: 09/336,536
 PRIOR FILING DATE: 1999-06-18
 PRIOR APPLICATION NUMBER: 09/342,687
 PRIOR FILING DATE: 1999-06-29
 PRIOR APPLICATION NUMBER: 09/345,464
 PRIOR FILING DATE: 1999-06-30
 PRIOR APPLICATION NUMBER: 09/365,164
 PRIOR FILING DATE: 1999-07-30
 PRIOR APPLICATION NUMBER: 09/399,723
 PRIOR FILING DATE: 1999-09-20
 PRIOR APPLICATION NUMBER: 09/409,634
 PRIOR FILING DATE: 1999-09-30
 PRIOR APPLICATION NUMBER: 09/471,179
 PRIOR FILING DATE: 1999-12-23
 PRIOR APPLICATION NUMBER: 09/474,071
 PRIOR FILING DATE: 1999-12-29
 PRIOR APPLICATION NUMBER: 09/474,072
 PRIOR FILING DATE: 1999-12-29
 PRIOR APPLICATION NUMBER: 09/514,010
 PRIOR FILING DATE: 2000-02-25
 PRIOR APPLICATION NUMBER: 09/516,745
 PRIOR FILING DATE: 2000-03-01
 PRIOR APPLICATION NUMBER: 09/572,002
 PRIOR FILING DATE: 2000-05-14
 PRIOR APPLICATION NUMBER: 09/597,993
 PRIOR FILING DATE: 2000-06-19
 PRIOR APPLICATION NUMBER: 09/599,596
 PRIOR FILING DATE: 2000-06-22
 PRIOR APPLICATION NUMBER: 09/630,334
 PRIOR FILING DATE: 2000-07-31
 PRIOR APPLICATION NUMBER: 09/606,565
 PRIOR FILING DATE: 2000-06-29
 PRIOR APPLICATION NUMBER: 09/606,317
 PRIOR FILING DATE: 2000-06-29
 PRIOR APPLICATION NUMBER: 09/665,666
 PRIOR FILING DATE: 2000-09-20
 PRIOR APPLICATION NUMBER: 09/677,751
 PRIOR FILING DATE: 2000-09-30
 NUMBER OF SEQ ID NOS: 162
 SEQ ID NO 55
 LENGTH: 969
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (6)...(761)
 US-09-796-753-55

Query Match 60.8%; Score 803.2; DB 11; Length 969;
 Best Local Similarity 99.6%; Pred. No. 8.4e-168;
 Matches 805; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	514	GGAGATCAGGAGCTGGAGATTGTTCAATCATCATCTGCTGGTGGTATATATGATAT	573
DB	2	GGAGATGGGGAGGAGCTGGAGATTGTTCAATCATCATCTGCTGGTGGTATATGATAT	61
QY	574	GGTGGTGGTATACAGCTGCTGCTGAGCAGTACAGAGCTGTGACAGGCTTCTATCAG	633
DB	62	GGTGGTGGTATACAGCTGCTGCTGAGCAGTACAGAGCTGTGACAGGCTTCTATCAG	121
QY	634	CCGGACACAGCCAGGGGGGAGAGAGAGATGCTGCTTCTAGAGAGATGCTTGCGCC	693
DB	122	CCGGACACAGCCAGGGGGGAGAGAGAGATGCTGCTTCTAGAGAGATGCTTGCGCC	181
QY	694	CTCGAGAGACAGATGTATGAGCAAGGATATCCAGAGCCGAGGCTTACGCCGCCCTCG	753
DB	182	CTCGAGAGACAGATGTATGAGCAAGGATATCCAGAGCCGAGGCTTACGCCGCCCTCG	241
QY	754	GCCACCGAGCCGCTGGCGCTGCGCCCTTCCGCCAGCGGAGCGCTTCCAGCGTTCCA	813
DB	242	GCCACCGAGCCGCTGGCGCTGCGCCCTTCCGCCAGCGGAGCGCTTCCAGCGTTCCA	301
QY	814	GCCACCTATTCGCTATCTGACAGCAGAGATGCACTGCGCACCCACCATCTGCTGTACA	873
DB	302	GCCACCTATTCGCTATCTGACAGCAGAGATGCACTGCGCACCCACCATCTGCTGTACA	361
QY	874	CGGGGAGAGCCGCCACCTTACAGAGGGGCCCTGACCTTCAAGCTTGGGAGCCCGAGCA	933
DB	362	CGGGGAGAGCCGCCACCTTACAGAGGGGCCCTTCAAGCTTGGGAGCCCGAGCA	421
QY	934	GCAGCTGGAATGAACCGGAGAGTGGTGGCGGACCCCAACAGAACCATCTTGACAG	993
DB	422	GCAGCTGGAATGAACCGGAGAGTGGTGGCGGACCCCAACAGAACCATCTTGACAG	481
QY	994	TGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1053
DB	482	TGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	541
QY	1054	CAGCGCCAGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1113
DB	542	CAGCGCCAGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	601
QY	1114	GGTATCGGCGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1173
DB	602	GGTATCGGCGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	661
QY	1174	CTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1233
DB	662	CTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	721
QY	1234	CTGGAGCAAGAGAGAGATTAACAGAAAGAGACCTCTCTAGAGGCTCCCGAGGGGGCGG	1293
DB	722	CTGGAGCAAGAGAGAGATTAACAGAAAGAGACCTCTCTAGAGGCTCCCGAGGGGGCGG	781
QY	1294	GGCTGGGGCTGCTAGGTGATAAAGCAG 1321	
DB	782	GGCTGGGGCTGCTAGGTGATAAAGCAG 809	

RESULT 5
 US-10-301-822-208
 Sequence 208, Application US/10301822
 Publication No. US20030148410A1
 GENERAL INFORMATION:
 APPLICANT: Millennium Pharmaceuticals, Inc.
 APPLICANT: Berger, Allison
 APPLICANT: Guillemette, Tracy L.
 APPLICANT: Kamatkar, Shubhangi
 APPLICANT: Schlegel, Robert
 APPLICANT: Monahan, John E.
 APPLICANT: Thibodeau, Stephen N.

APPLICANT: Burtart, Lawrence J.
 TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
 METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 THERAPY OF COLON CANCER
 FILE REFERENCE: MPM01-029P2RNM
 CURRENT APPLICATION NUMBER: US/10/301,822
 PRIOR FILING DATE: 2002-11-21
 PRIOR APPLICATION NUMBER: US 60/339,971
 PRIOR FILING DATE: 2001-12-10
 PRIOR APPLICATION NUMBER: US 60/361,978
 PRIOR FILING DATE: 2002-03-05
 PRIOR APPLICATION NUMBER: US 60/381,988
 PRIOR FILING DATE: 2002-05-20
 NUMBER OF SEQ IDS: 228
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 208
 LENGTH: 1141
 TYPE: DNA
 ORGANISM: Homo Sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (96)...(854)
 US-10-301-822-208

Query Match 60.7%; Score 802.2; DB 12; Length 1141;
 Best Local Similarity 98.4%; Pred. No. 1.4e-167;
 Matches 810; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

499 TTTGTTCCAGAGCATGAGATCAGGAGCTGAGCTGTTGTTGATCATCATCATGCTGT 558
 77 TCTCTGGAAGAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 136
 559 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 618
 137 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 196
 619 ACGGTCCTTCATCAGCCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 678
 197 ACGGTCCTTCATCAGCCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 256
 679 AGGATGCTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 738
 257 AGGATGCTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 316
 739 CTACGCCCCGCTCGGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 798
 317 CTACGCCCCGCTCGGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 376
 799 CTTCACCGCTTCACAGCCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 858
 377 CTTCACCGCTTCACAGCCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 436
 859 CATGCGCTGTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 918
 437 CATGCGCTGTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 496
 919 TCGGAGCCCCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 978
 497 TCGGAGCCCCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 556
 979 AACCATCTTCGACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1038
 557 AACCATCTTCGACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 616
 1039 CAGTAACTCGGAGCATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1098
 617 CAGTAACTCGGAGCATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 676
 1099 GCCCAGCTTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1158
 677 GCCCAGCTTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 736
 1159 CAGTGGGCGGCTCTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1218

737 CAGTGGGCGGCTCTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 796
 1219 AGAGAGCGAGCATCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1278
 797 AGAGAGCGAGCATCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 856
 1279 TCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1321
 857 TCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 899

RESULT 6

US-10-205-823-412
 Sequence 412, Application US/10205823
 Publication No. US20030108963A1

GENERAL INFORMATION:
 APPLICANT: Schlegel, Robert
 APPLICANT: Monahan, John E.
 APPLICANT: Endege, Wilson O.
 APPLICANT: Gannavarapu, Manjula
 APPLICANT: Gorbacheva, Bella
 APPLICANT: Hoersch, Sebastian
 APPLICANT: Kamalakar, Shudhangl
 APPLICANT: Monsey, Angela M.
 APPLICANT: Glat, Karen
 APPLICANT: Zhao, Xumei
 APPLICANT: Anderson, Dustin

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
 METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 THERAPY OF PROSTATE CANCER
 FILE REFERENCE: MRI-044

CURRENT APPLICATION NUMBER: US/10/205,823
 PRIOR FILING DATE: 2002-07-25

PRIOR APPLICATION NUMBER: 60/307,982
 PRIOR FILING DATE: 2001-07-25

PRIOR APPLICATION NUMBER: 60/314,356
 PRIOR FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/325,020
 PRIOR FILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: 60/341,746
 PRIOR FILING DATE: 2001-12-12

PRIOR APPLICATION NUMBER: 60/362,158
 PRIOR FILING DATE: 2002-03-05

NUMBER OF SEQ IDS: 455
 SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 412
 LENGTH: 1141
 TYPE: DNA

ORGANISM: Homo sapiens
 US-10-205-823-412

Query Match 60.7%; Score 802.2; DB 14; Length 1141;
 Best Local Similarity 98.4%; Pred. No. 1.4e-167;
 Matches 810; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

499 TTTGTTCCAGAGCATGAGATCAGGAGCTGAGGTTGTTGATCATCATCATGCTGT 558
 77 TCTCTGGAAGAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 136
 559 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 618
 137 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 196
 619 ACGGTCCTTCATCAGCCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 678
 197 ACGGTCCTTCATCAGCCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 256
 679 AGGATGCTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 738
 257 AGGATGCTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 316
 739 CTACGCCCCGCTCGGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 798

```

Db      317 CTACGCCCCGCTGGGCCACCGACCGCTGCGCTGCGCCCTTCCGCCAGCGGGAGCG 376
QY      799 CTTCACCGCTTCCACGCCACCTTATCCGTATCTTGACACAGAGATGACCTGCACCCAC 858
Db      377 CTTCACCGCTTCCACGCCACCTTATCCGTATCTTGACACAGAGATGACCTGCACCCAC 436
QY      859 CATCTGCTGTACAGCGGGAGAGAGCCCAACCTTACAGAGGCCCTTGACACCTTCAGCT 918
Db      437 CATCTGCTGTACAGCGGGAGAGAGCCCAACCTTACAGAGGCCCTTGACACCTTCAGCT 496
QY      919 TCGGAGACCCGAGAGAGAGCTGGAATGAACCGGAGTCTGCTGCGGACACCCCAAAACAG 978
Db      497 TCGGAGACCCGAGAGAGAGCTGGAATGAACCGGAGTCTGCTGCGGACACCCCAAAACAG 556
QY      979 AACCATCTTCAGAGTACCTGTATGATGTGTCAGAGCTGGGCGGCCCTTGCCCCCAG 1038
Db      557 AACCATCTTCAGAGTACCTGTATGATGTGTCAGAGCTGGGCGGCCCTTGCCCCCAG 616
QY      1039 CAGTAACTCGGGCATACGCGCCACGTGTACGCGACGCGGGCGCATGAGGGGCGCGC 1098
Db      617 CAGTAACTCGGGCATACGCGCCACGTGTACGCGACGCGGGCGCATGAGGGGCGCGC 676
QY      1099 GCCCACCCTACAGAGAGTATCGGCGCATACCGGGGCTCTCTTCACAGACACAGAG 1158
Db      677 GCCCACCCTACAGAGAGTATCGGCGCATACCGGGGCTCTCTTCACAGACACAGAG 736
QY      1159 CAGTGGCGCGCTCTCTCTCTGAGAGGAGACCGGCTCCACACACACATCGGCGCT 1218
Db      737 CAGTGGCGCGCTCTCTCTCTGAGAGGAGACCGGCTCCACACACACATCGGCGCT 796
QY      1219 AGAGAGCGCAGCCTATGAGAGCAAAAGAGATGAAGAAAGAGACACCTCTCTAGGG 1278
Db      797 AGAGAGCGCAGCCTATGAGAGCAAAAGAGATGAAGAAAGAGACACCTCTCTAGGG 856
QY      1279 TCCCGAGGGGGCGCGCTGGGCGCTGCTAGAGTGAAGAGCGAG 1321
Db      857 TCCCGAGGGGGCGCGCTGGGCGCTGCTAGAGTGAAGAGCGAG 899

```

RESULT 7 US-10-241-220-44

```

; Sequence 44, Application US/10241220
; Publication No. US20030148408A1
; GENERAL INFORMATION:
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zhenlin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5010R1-US
; CURRENT APPLICATION NUMBER: US/10/241,220
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 44
; LENGTH: 1850
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-241-220-44

```

Query Match 60.7%; Score 802.2; DB 12; Length 1850;
Best Local Similarity 98.4%; Pred. No. 1.4e-167;

Matches 810; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

```

QY      499 TTTGTTCCAGAGCATGAGATGAGAGCTGAGCTTGTTCATGATCATCATCTGCT 558
Db      77 TCTCCTGGCAAAACAGCAATGCGGAGCTGAGTTGTCATGATCATCATCTGCT 136

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QY      559 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 618
Db      137 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 196
QY      619 ACGGTCTTTCATCAGCGCGGACACCGAGGGGCGGAGAGAGAGATGCTCTCAGAG 678
Db      197 ACGGTCTTTCATCAGCGCGGACACCGAGGGGCGGAGAGAGAGATGCTCTCAGAG 256
QY      679 AGGATGCTGTGGCCCTTCGAGAGACACAGTGTGAGCAAGGAAATCCAGAGCGGAGCT 738
Db      257 AGGATGCTGTGGCCCTTCGAGAGACACAGTGTGAGCAAGGAAATCCAGAGCGGAGCT 316
QY      739 CTAGCGCCCGCTGGGCGCCACCGAGCCCTGCGCTGCGCCCTTGGCCAGCGGGAGCG 798
Db      317 CTAGCGCCCGCTGGGCGCCACCGAGCCCTGCGCTGCGCCCTTGGCCAGCGGGAGCG 376
QY      799 CTTCACCGCTTCCAGCGCCACCTATCCGTATCTGTCAGACAGAGATGACCTGCACCCAC 858
Db      377 CTTCACCGCTTCCAGCGCCACCTATCCGTATCTGTCAGACAGAGATGACCTGCACCCAC 436
QY      859 CATCTGCTGTACAGCGGGAGAGAGCCCGACCTTACAGAGGGCCCTGACACCTTCAGCT 918
Db      437 CATCTGCTGTACAGCGGGAGAGAGCCCGACCTTACAGAGGGCCCTGACACCTTCAGCT 496
QY      919 TCGGAGACCCGAGACAGAGCTGGAATGAACCGGAGTGTGAGGCGGACCCCAAAACAG 978
Db      497 TCGGAGACCCGAGACAGAGCTGGAATGAACCGGAGTGTGAGGCGGACCCCAAAACAG 556
QY      979 AACCATCTTCAGAGTACCTGTATGATGTGTCAGAGCTGGGCGGCCCTTGCCCCCAG 1038
Db      557 AACCATCTTCAGAGTACCTGTATGATGTGTCAGAGCTGGGCGGCCCTTGCCCCCAG 616
QY      1039 CAGTAACTCGGGCATACGCGCCACGTGTACGCGACGCGGGGCGCATGAGGGGCGCGC 1098
Db      617 CAGTAACTCGGGCATACGCGCCACGTGTACGCGACGCGGGGCGCATGAGGGGCGCGC 676
QY      1099 GCCCACCCTACAGAGAGTATCGGCGCATACCGGGGCTCTCTTCACAGACACAGAG 1158
Db      677 GCCCACCCTACAGAGAGTATCGGCGCATACCGGGGCTCTCTTCACAGACACAGAG 736
QY      1159 CAGTGGCGCGCTCTCTCTCTGAGAGGAGACCGGCTCCACACACACATCGGCGCT 1218
Db      737 CAGTGGCGCGCTCTCTCTCTGAGAGGAGACCGGCTCCACACACACATCGGCGCT 796
QY      1219 AGAGAGCGCAGCCTATGAGAGCAAAAGAGATGAAGAAAGAGACACCTCTCTAGGG 1278
Db      797 AGAGAGCGCAGCCTATGAGAGCAAAAGAGATGAAGAAAGAGACACCTCTCTAGGG 856
QY      1279 TCCCGAGGGGGCGCGCTGGGCGCTGCTAGAGTGAAGAGCGAG 1321
Db      857 TCCCGAGGGGGCGCGCTGGGCGCTGCTAGAGTGAAGAGCGAG 899

```

RESULT 8 US-10-098-841-71

```

; Sequence 71, Application US/10098841
; Publication No. US20020197679A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Xu, Chongjun
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungling
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Duntai
; APPLICANT: Wang, Zhilwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Qian, Xiaohong B.

```


Db 825 GCGCCGACAGGCTACGCCCCCGCTCGGCCACGACGCGCTGGCCGCTCCGCTTCCG 884
Qy 788 CAGCGGAGAGCGCTTCCACGCGCTTCCAGCCACCTTACCTTACCTGACAGAGATCGAC 847
Db 885 CAGCGGAGAGCGCTTCCACGCGCTTCCAGCCACCTTACCTTACCTGACAGAGATCGAC 944
Qy 848 CTGCGACCCAGCATCTGCTGTGACAGCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 907
Db 945 CTGCGACCCAGCATCTGCTGTGACAGCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1004
Qy 908 ACCCTCCAGCTTGGGAG 967
Db 1005 ACCCTCCAGCTTGGGAG 1064
Qy 968 CCCCCAACAGACAGCATCTTGGACAGTACCTGATGATGATGATGATGATGATGATGATGATG 1027
Db 1065 CCCCCAACAGACAGCATCTTGGACAGTACCTGATGATGATGATGATGATGATGATGATGATG 1124
Qy 1028 TGCCCCCGACAGTACCTGAGGAGATGACGCGGACGCTGACGAGCGGGGCGGCGATG 1087
Db 1125 TGCCCCCGACAGTACCTGAGGAGATGACGCGGACGCTGACGAGCGGGGCGGCGATG 1184
Qy 1088 GAGGGGGCGCGCCACCTACAG 1147
Db 1185 GAGGGGGCGCGCCACCTACAG 1244
Qy 1148 CACGACAGACAGATGAGGAG 1207
Db 1245 CACGACAGACAGATGAGGAG 1304
Qy 1208 ATCGCGCCCTTAG 1267
Db 1305 ATCGCGCCCTTAG 1364
Qy 1268 CCTCTTAGGAGTCCCGAGGGGGCGGGGCTGGGAGTGGTGAAGAAAGGAG 1321
Db 1365 CCTCTTAGGAGTCCCGAGGGGGCGGGGCTGGGAGTGGTGAAGAAAGGAG 1418

RESULT 12

US-09-934-249-14/c
; Sequence 14, Application US/09934249
; Patent No. US20020115081A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Richard T.
; APPLICANT: Landschulz, Katherine T.
; APPLICANT: Turi, Thomas G.
; APPLICANT: Thompson, John F.
; APPLICANT: Kennedy, Scott P.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: P0738/7001/ERP/KA
; CURRENT APPLICATION NUMBER: US/09/934,249
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/227,159
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 693
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (639)..
; OTHER INFORMATION: a, c, g, or t/u
US-09-934-249-14

Query Match 37.4%; Score 493.6; DB 10; Length 693;
Best Local Similarity 97.4%; Pred. No. 1.2e-99;
Matches 533; Conservative 0; Mismatches 10; Indels 4; Gaps 3;

Qy 776 CCGCCCTTCCGCGGAGGAGCGCTTCCACGCGCTTCCAGCCGACCTATCCGATCTGACG 835

Db 693 CCGCCCTTCCGCGGAGGAGCGCTTCCACGCGCTTCCAGCCGACCTATCCGATCTGACG 634
Qy 836 CACGAGATGAGAGCTTCCAGCCGACCTATCTGCTGTAGAGAGAGAGAGAGAGAGAGAGAGAG 895
Db 633 CACGAGATGAGAGCTTCCAGCCGACCTATCTGCTGTAGAGAGAGAGAGAGAGAGAGAGAGAG 577
Qy 896 CAGGAGCCCTTCCAGCCGACCTATCTGCTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 955
Db 576 CAGGAGCCCTTCCAGCCGACCTATCTGCTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 517
Qy 936 TCGGTGCGGAG 1015
Db 516 TCGGTGCGGAG 457
Qy 1016 TCGGTGCGGAG 1075
Db 456 TCGGTGCGGAG 397
Qy 1076 GCGGGGCGCATGAG 1135
Db 396 GCGGGGCGCATGAG 337
Qy 1136 TCGGTGCGGAG 1194
Db 336 TCGGTGCGGAG 277
Qy 1195 CACGACAGACAGATGAGGAG 1254
Db 276 CCGCCACAGACAGATGAGGAG 217
Qy 1255 ACAGAAAGAGACAGCTTCTTAGAGTCCCGAGGGGGCGGGGCTGGGAGTGGTGAAGTGA 1314
Db 216 ACAGAAAGAGACAGCTTCTTAGAGTCCCGAGGGGGCGGGGCTGGGAGTGGTGAAGTGA 157
Qy 1315 AAGGAG 1321
Db 156 AAGGAG 150

RESULT 13

US-09-796-753-57
; Sequence 57, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723

PRIOR FILING DATE: 1999-09-20
 PRIOR APPLICATION NUMBER: 09/409,634
 PRIOR FILING DATE: 1999-09-30
 PRIOR APPLICATION NUMBER: 09/471,179
 PRIOR FILING DATE: 1999-12-23
 PRIOR APPLICATION NUMBER: 09/474,071
 PRIOR FILING DATE: 1999-12-29
 PRIOR APPLICATION NUMBER: 09/474,072
 PRIOR FILING DATE: 1999-12-29
 PRIOR APPLICATION NUMBER: 09/514,010
 PRIOR FILING DATE: 2000-02-25
 PRIOR APPLICATION NUMBER: 09/516,745
 PRIOR FILING DATE: 2000-03-01
 PRIOR APPLICATION NUMBER: 09/572,002
 PRIOR FILING DATE: 2000-05-14
 PRIOR APPLICATION NUMBER: 09/597,993
 PRIOR FILING DATE: 2000-06-19
 PRIOR APPLICATION NUMBER: 09/599,596
 PRIOR FILING DATE: 2000-06-22
 PRIOR APPLICATION NUMBER: 09/630,334
 PRIOR FILING DATE: 2000-07-31
 PRIOR APPLICATION NUMBER: 09/606,565
 PRIOR FILING DATE: 2000-06-29
 PRIOR APPLICATION NUMBER: 09/606,317
 PRIOR FILING DATE: 2000-06-29
 PRIOR APPLICATION NUMBER: 09/665,666
 PRIOR FILING DATE: 2000-09-20
 PRIOR APPLICATION NUMBER: 09/677,751
 PRIOR FILING DATE: 2000-09-30
 NUMBER OF SEQ ID NOS: 162
 SEQ ID NO 57
 LENGTH: 1713
 TYPE: DNA
 ORGANISM: Mouse
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (2)...(652)
 US-09-796-753-57

Query Match 35.3%; Score 466.2; DB 11; Length 1713;
 Best Local Similarity 83.9%; Pred. No. 1.3e-93;
 Matches 573; Conservative 0; Mismatches 83; Indels 27; Gaps 3;

QY 595 GGTGAGGCACTACAGAGTGTCTGCAAGGCTCTTCATACAGCGGACAGAGGCGGAG 654
 DB 1 GCTGAGGCACTACAGAGTGTCTGCAAGGCTCTTCATACAGCGGACAGAGGCGGAG 60
 QY 655 GAGAGAGATGCGCTGTCTCTCAGAGAGATGCTGTGCGCTCTGAGAGAGAGAGAGAG 714
 DB 61 GAGAGAGATGAGTGTCTCTGAGAGAGATGCTGTGCGCTCTGAGAGAGAGAGAGAG 120
 QY 715 CAACGGAATCCGAGAGCGGAGGTCATACGCGCGCTCGGCGCAGCGAGCGCTGCGCT 774
 DB 121 ---TGGAATCGCGAGGAGGAGGTCATGCGCGCTCGGCGCAGCGAGCGAGCTGCTG 177
 QY 775 GCGCGCTTCGCGAGGAGGAGGCTTCACGCGCTTCGAGCGGCGCAGCGAGCGCTGCGCT 834
 DB 178 GCGCGCTTCATCAGAGG-----AGCGATTCAGAGCGGCGCAGCGAGCGCTGCGCT 228
 QY 835 GCAAGAGATGAGCTTCGAGCGGAGGTCATGCTGTGAGAGAGGAGAGAGCGGCGGAG 894
 DB 229 GCAAGAGATGAGCTTCGAGCGGAGGTCATGCTGTGAGAGAGAGAGAGAGCGGCGGAG 288
 QY 895 CCAAGGCGCGCTTCAGAGCTTCAGAGTGTGAGAGCGGAGAGAGAGAGAGAGAGAGAG 954
 DB 289 CCAAGGCGCGCTTCAGAGCTTCAGAGTGTGAGAGCGGAGAGAGAGAGAGAGAGAGAG 348
 QY 955 GTCTGAGCGGAGCGGAG 1014
 DB 349 ATGTGTGAGCGGAGCGGAG 408
 QY 1015 GCTGAGGCGGCGCTTCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1074

DB 409 GCTGAGGCGGCGCTTCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 468
 QY 1075 CGCGGCGGCGGAG 1134
 DB 469 CGGTGCGGCGGAG 528
 QY 1135 GTCTGAGCGGAG 1194
 DB 529 CTCTGAGCGGAG 588
 QY 1195 CCACGAG 1254
 DB 589 CCATGAG 633
 QY 1255 ACAG 1277
 DB 634 ACAG 656

RESULT 14
 US-09-934-249-16
 Sequence 16, Application US/09934249
 Patent No. US20020115081A1
 GENERAL INFORMATION:
 APPLICANT: Lee, Richard T.
 APPLICANT: Landschultz, Katherine T.
 APPLICANT: Turt, Thomas G.
 APPLICANT: Thompson, John F.
 APPLICANT: Kennedy, Scott P.
 TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
 FILE REFERENCE: P0738/7001/ERP/KA
 CURRENT APPLICATION NUMBER: US/09/934,249
 PRIOR FILING DATE: 2001-08-21
 PRIOR APPLICATION NUMBER: US 60/227,159
 PRIOR FILING DATE: 2000-08-22
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 16
 LENGTH: 8093
 TYPE: DNA
 ORGANISM: Homo Sapiens
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (6477)...(6477)
 OTHER INFORMATION: c or t/u
 NAME/KEY: unsure
 LOCATION: (6837)...(6837)
 OTHER INFORMATION: a or c
 US-09-934-249-16

Query Match 26.4%; Score 349; DB 10; Length 8093;
 Best Local Similarity 73.7%; Pred. No. 7.9e-68;
 Matches 474; Conservative 0; Mismatches 160; Indels 9; Gaps 2;

QY 522 CGAGCTGAGAGTTGTCAGATCATCATCATGCTGTGATGATGATGATGATGATGATG 581
 DB 250 CGAGCTGAGAGTTGTCAGATCATCATCATGCTGTGATGATGATGATGATGATGATG 309
 QY 582 TGATCATGCTGCTGTGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 641
 DB 310 TGATCATGCTGCTGTGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 369
 QY 642 GCCAGGCGGAG 701
 DB 370 ACCAGAGCGGAG 429
 QY 702 GCACAGTGTAG 761
 DB 430 CGCGCGGAG 483
 QY 762 ACCGCTGAGCGGAG 821

Db	484	ACAGGTTCCAGCGCCGTCCTTCATCCAGAGGGAGTCGTTACAGCGCGTTCCAGGCCACT	543
OY	822	ATCCGTACCTGCAGCAGCATGCAGCTGCCACCCACCATCTCGCTGTACAGCGGGAG	881
Db	544	ACCCCTATGTGCAGCAGCATGTGATCTCTCCACCATCTCCCTGTCGCCAGGTGAAG	603
OY	882	AGCCCCACCCCTAACCGAGGGCCCTGCACCCCTCCACCTTCGCGGACCCCGACGACGACGTGG	941
Db	604	AGCCACCTCTTACCGAGGGGCCCTGCACCCCTGCACCTCCGGGACCTGAAACGACGATGG	663
OY	942	AACGTAAACCGGGAGTCTGCGCGCACCCCAACAGAACCATCTTCGACAGTGCATGA	1001
Db	664	AACCTAACCGAGAGTCCGTGAGGGGCCCAACCAACGAAACCATATTGACAGTGAATTGA	723
OY	1002	TGGAATAGTGCCAGG---CTGGGCGGGCCCTGCCCCCAGCAGCATCTCGGGCATCAGCG	1056
Db	724	TAGACATTTGCTATGTATGATAGCGGGGGTCCATGCCCCACCGACGAGCAACTCGGGCATCAGTG	783
OY	1059	CCAGCTGTACGGCAGCGCGCGGGGCCCATGTGAGAGGGGCCCGGCCCACTACAGCAGAGTCA	1111
Db	784	CAAGCACCTTGAGCAGCATGAACGGGAGATGAGGGGGCCACCCCCACATACACCGAGGTTGA	843
OY	1119	TCGGCACATACCCGGGGTCTCTCTCTTCACGACACAGCAGAGCAG	1161
Db	844	TGGGCGACACCCACGAGCGCGCTCTTCTCTTCACATCACAGCGCAG	886

RESULT 5
 US-09-934-249-15
 Sequence 15, Application US/09934249
 Patent No. US20020115081A1
 GENERAL INFORMATION:
 APPLICANT: Lee, Richard T.
 APPLICANT: Landschulz, Katherine T.
 APPLICANT: Turti, Thomas G.
 APPLICANT: Thompson, John F.
 APPLICANT: Kennedy, Scott P.
 TITLE OF INVENTION: DIAGNOSIS AND TREATMENT
 TITLE OF INVENTION: CARDIOVASCULAR CONDIDME
 FILE REFERENCE: P0738/7001/ERS/KA
 CURRENT APPLICATION NUMBER: US/09/934,249
 CURRENT FILING DATE: 2001-08-21
 PRIOR APPLICATION NUMBER: US 60/227,159
 PRIOR FILING DATE: 2000-08-22
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: FastSeq for Windows Version 3.0.
 SEQ ID NO 15
 LENGTH: 475
 TYPE: DNA
 ORGANISM: Mus Musculus
 US-09-934-249-15

Query Match	25.9%;	Score 341.8;	DB 10;	Length 475;
Best Local Similarity	85.5%;	Pred. No. 3e-66;		
Matches 408; Conservative	0;	Mismatches 57;	Indels 12;	Gaps 2

[illegible]

Db 251 AGAGACGATGGACTGTCTCTGGAGAGATGCTTCTGGCCCTCAGAGAGTACGGTGTACAGG- 309Y
 Oy 716 AAGAGATCCACAGACGCCGACGGTCTACGCCCCGCTCGACACAGACCGCGTGGCCGTG 775Y
 Db 310 --TGGATGCGGAGGACACAGGCTTAGTGCCCCGCTCGACACAGTACCGACGATGGCGTGTG 367Y
 Oy 776 CCGCCCTTGCGCCAGCGGGAGCGCTTCACCGCTTCACGACCACTATCCGTACTCTGACG 835Y
 Db 368 CCCCCCTTATCCAGGG-----AGCGATTCACACCACTTACCTTACTCTCAG 418Y
 Oy 836 CACGAGATCGACCTGCGACACCAACCAATCTTGCTGCAGAGGGGAGAGACCCCAACC 892Y
 Db 419 CAGAGAAATTGCCCTGGCACCAACCAACACTTACTGTGTGATGGGGAGAGACCCCAACC 475Y

Search completed: August 27, 2003, 21:35:09
Job time : 390 secs

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